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(54) Title: ANTIMICROBIAL PROTEINS (57) Abstract <p>A new family of antimicrobial proteins is described. Prototype proteins can be isolated from <i>Macadamia integrifolia</i> as well as other plant species. DNA encoding the protein is also described as well as DNA constructs which can be used to express the antimicrobial protein or to introduce the antimicrobial protein into a plant. Compositions comprising the antimicrobial proteins or the antimicrobial protein <i>per se</i> can be administered to plants or mammalian animals to combat microbial infestation.</p>		

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ANTIMICROBIAL PROTEINS

TECHNICAL FIELD

This invention relates to isolated proteins which exert inhibitory activity on the growth of fungi and bacteria, which fungi and bacteria include some microbial pathogens of plants and animals.

5 The invention also relates to recombinant genes which include sequences encoding the proteins, the expression products of which recombinant genes can contribute to plant cells or cells of other organism's defence against invasion by microbial pathogens. The invention further relates to the use of the proteins and/or genes encoding the proteins for the control of microbes in human and veterinary clinical conditions.

10 BACKGROUND ART

Microbial diseases of plants are a significant problem to the agricultural and horticultural industries. Plant diseases in general cause millions of tonnes of crop losses annually with fungal and bacterial diseases responsible for significant portions of these losses. One possible way of combating fungal and bacterial diseases is to provide transgenic plants capable of expressing a

15 protein or proteins which in some way increase the resistance of the plant to pathogen attack. A simple strategy is to first identify a protein with antimicrobial activity *in vitro*, to clone or synthesise the DNA sequence encoding the protein, to make a chimaeric gene construct for efficient expression of the protein in plants, to transfer this gene to transgenic plants and to assess the effect of the introduced gene on resistance to microbial pathogens by comparison with control plants.

20 The first and most important step in the strategy for disease control described above is to identify, characterise and describe a protein with strong antimicrobial activity. In recent years, many different plant proteins with antimicrobial and/or antifungal activity have been identified and described. These proteins have been categorised into several classes according to either their presumed mode of action and/or their amino acid sequence homologies. These classes include the

25 following: chitinases (Roberts, W.K. *et al.* [1986] *Biochim. Biophys. Acta* 880:161-170); β -1,3-glucanases (Manners, J.D. *et al.* [1973] *Phytochemistry* 12:547-553); thionins (Bolmann, H. *et al.* [1988] *EMBO J.* 7:1559-1565 and Fernandez de Caley, R. *et al.* [1972] *Appl. Microbiol.* 23:998-1000); permatins (Roberts, W. K. *et al.* [1990] *J. Gen. Microbiol.* 136:1771-1778 and Vigers, A.J. *et al.* [1991] *Mol. Plant-Microbe Interact.* 4:315-323); ribosome-inactivating proteins (Roberts, W. K. *et al.* [1986] *Biochim. Biophys. Acta* 880:161-170 and Leah, R. *et al.* [1991] *J. Biol. Chem.* 266:1564-1573); plant defensins (Terras, F. R. G. *et al.* [1995] *The Plant Cell* 7:573-588); chitin binding proteins (De Bolle, M.F.C. *et al.* [1992] *Plant Mol. Biol.* 22:1187-1190 and Van Parijs, J. *et al.* [1991] *Planta* 183:258-264); thaumatin-like, or osmotin-like proteins (Woloshuk, C.P. *et al.* [1991] *The Plant Cell* 3:619-628 and Hejgaard, J. [1991] *FEBS Letts.* 291:127-131); PR1-type

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proteins (Niderman, T. *et al.* [1995] *Plant Physiol.* 108:17-27.) and the non-specific lipid transfer proteins (Terras, F.R.G. *et al.* [1992] *Plant Physiol.* 100:1055-1058 and Molina, A. *et al.* [1993] *FEBS Letts.* 3166:119-122). Another class of antimicrobial proteins from plants is the knottin or knottin-like antimicrobial proteins (Cammue, B.P.A. *et al.* [1992] *J. Biol. Chem.* 67:2228-2233; 5 Broekaert W.F. *et al.* (1997) *Crit. Rev. in Plant Sci.* 16(3):297-323). A class of antimicrobial proteins termed 4-cysteine proteins has also been reported in the literature which class includes Maize Basic Protein (MBP-1) (Duvick, J.P. *et al.* [1992] *J. Biol. Chem.* 267:18114-18120). A novel antimicrobial protein which does not fit into any previously described class of antimicrobial proteins has also been isolated from the seeds of *Macadamia integrifolia* termed MiAMP1 (Marcus, J.P. *et al.* 10 [1997] *Eur. J. Biochem.* 244:743-749). In addition, plants are not the sole source of antimicrobial proteins and there are many reports of the isolation of antimicrobial proteins from animal and microbial cells (reviewed in Gabay, J.E. [1994] *Science* 264:373-374 and in "Antimicrobial peptides" [1994] *CIBA Foundation Symposium 186*, John Wiley and Sons Publ., Chichester, UK).

There is evidence that the ectopic expression of genes encoding proteins that have *in vitro* 15 antimicrobial activity in transgenic plants can result in increased resistance to microbial pathogens. Examples of this engineered resistance include transgenic plants expressing genes encoding: a plant chitinase, either alone (Brogli, K. *et al.* [1991] *Science* 254:1194-1197) or in combination with a β -1,3-glucanase (Van den Elzen, P.J.M. *et al.* [1993] *Phil. Trans. Roy. Soc.* 342:271-278); a plant defensin (Terras, F.R.G. *et al.* [1995] *The Plant Cell* 7:573-588); an osmotin-like protein (Liu, D. *et al.* [1994] *Proc. Natl. Acad. Sci. USA* 91:1888-1892); a PR1-class protein (Alexander, D. *et al.* 20 [1993] *Proc. Natl. Acad. Sci. USA* 90:7327-7331) and a ribosome-inactivating protein (Logemann, J. *et al.* [1992] *Bio/Technology* 10:305-308).

Although the potential use of antimicrobial proteins for engineering disease resistance in transgenic plants has been described extensively, there are other applications which are worthy of 25 mention. Firstly, highly potent antimicrobial proteins can be used for the control of plant disease by direct application (De Bolle, M.F.C. *et al.* [1993] in *Mechanisms of Plant Defence Responses*, B. Fritig and M. Legrand eds., Kluwer Acad. Publ., Dordrecht, NL, pp. 433-436). In addition, antimicrobial peptides have potential therapeutic applications in human and veterinary medicine. Although this has not been described for peptides of plant origin it is being actively explored with 30 peptides from animals and has reached clinical trials (Jacob, L. and Zasloff, M. [1994] in "Antimicrobial Peptides", *CIBA Foundation Symposium 186*, John Wiley and Sons Publ., Chichester, UK, pp. 197-223).

Antimicrobial proteins exhibit a variety of three-dimensional structures which will determine in large part the activity which they manifest. Many of the global structures exhibited by these

proteins have been determined (Broekaert W.F. *et al.* (1997) *Crit. Rev. in Plant Sci.* 16(3):297-323). A large factor in determining the stability of these proteins is the presence of disulfide bridges between various cysteines located in α -helical and β -sheet regions. Many peptides with toxic activity such as conotoxin are well known to be stabilized by disulfide bridges (see for example Hill, J.M. *et al.* (1996) *Biochemistry* 35(27): 8824-8835). In the case of the conotoxin referenced above, a compact structure is formed consisting of a helix, a small β -hairpin, a cis-hydroxyproline, and several turns. The molecule is stabilized by three disulfide bonds, two of which connect the α -helix and the β -sheet, forming a solid structural core. Interestingly, eight arginine and lysine side chains in this molecule project into the solvent in a radial orientation relative to the core of the molecule. These cationic side chains form potential sites of interaction with anionic sites on pathogen membranes (Hill, J.M. *et al. supra*).

The invention described herein constitutes previously undiscovered and thus novel proteins with antimicrobial activity. These proteins can be isolated from *Macadamia integrifolia* (Mi) seeds or from cotton or cocoa seeds. In addition, protein fragments which are antifungal can be derived from larger seed storage proteins containing regions of substantial similarity to the antimicrobial proteins from macadamia described here. Examples of seed storage proteins which contain regions similar to the proteins which have been purified can be seen in Figure 4. *Macadamia integrifolia* belongs to the family Proteaceae. *M. integrifolia*, also known as Bauple Nut or Queensland Nut, is considered by some to be the world's best edible nut. Cotton (*Gossypium hirsutum*) belongs to the family Malvaceae and is cultivated extensively for its fiber. Cocoa (*Theobroma cacao*) belongs to the family Sterculiaceae and is used around the world for a wide variety of cocoa products.

The fact that both the macadamia and cocoa antimicrobial proteins are found in edible portions of these plants makes these peptides attractive for use in genetic engineering for disease resistance since transgenic plants expressing these proteins are unlikely to show added toxicity. Proteins may also be safe for human and veterinary use.

SUMMARY OF THE INVENTION

According to a first embodiment of the invention, there is provided a protein fragment having antimicrobial activity, wherein said protein fragment is selected from:

- (i) a polypeptide having an amino acid sequence selected from:

residues 29 to 73 of SEQ ID NO: 1
residues 74 to 116 of SEQ ID NO: 1
residues 117 to 185 of SEQ ID NO: 1
residues 186 to 248 of SEQ ID NO: 1
residues 29 to 73 of SEQ ID NO: 3

- residues 74 to 116 of SEQ ID NO: 3
 residues 117 to 185 of SEQ ID NO: 3
 residues 186 to 248 of SEQ ID NO: 3
 residues 1 to 32 of SEQ ID NO: 5
 5 residues 33 to 75 of SEQ ID NO: 5
 residues 76 to 144 of SEQ ID NO: 5
 residues 145 to 210 of SEQ ID NO: 5
 residues 34 to 80 of SEQ ID NO: 7
 residues 81 to 140 of SEQ ID NO: 7
 10 residues 33 to 79 of SEQ ID NO: 8
 residues 80 to 119 of SEQ ID NO: 8
 residues 120 to 161 of SEQ ID NO: 8
 residues 32 to 91 of SEQ ID NO: 21
 residues 25 to 84 of SEQ ID NO: 22
 15 residues 29 to 94 of SEQ ID NO: 24
 residues 31 to 85 of SEQ ID NO: 25
 residues 1 to 23 of SEQ ID NO: 26
 residues 1 to 17 of SEQ ID NO: 27
 residues 1 to 28 of SEQ ID NO: 28;
- 20 (ii) a homologue of (i);
 (iii) a polypeptide containing a relative cysteine spacing of C-2X-C-3X-C-(10-12)X-C-3X-C-3X-C wherein X is any amino acid residue, and C is cysteine;
 (iv) a polypeptide containing a relative cysteine and tyrosine/phenylalanine spacing of Z-2X-C-3X-C-(10-12)X-C-3X-C-3X-Z wherein X is any amino acid residue, and C is
 25 cysteine, and Z is tyrosine or phenylalanine;
 (v) a polypeptide containing a relative cysteine spacing of C-3X-C-(10-12)X-C-3X-C wherein X is any amino acid residue, and C is cysteine;
 (vi) a polypeptide with substantially the same spacing of positively charged residues relative to the spacing of cysteine residues as (i); and
 30 (vii) a fragment of the polypeptide of any one of (i) to (vi) which has substantially the same antimicrobial activity as (i).

According to a second embodiment of the invention, there is provided a protein containing at least one polypeptide fragment according to the first embodiment, wherein said polypeptide fragment

has a sequence selected from within a sequence comprising SEQ ID NO: 1, SEQ ID NO: 3 or SEQ ID NO: 5.

According to a third embodiment of the invention, there is provided a protein having a sequence selected from SEQ ID NO: 1, SEQ ID NO: 3 or SEQ ID NO: 5.

5 According to a fourth embodiment of the invention, there is provided an isolated or synthetic DNA encoding a protein according to the first embodiment

According to a fifth embodiment of the invention, there is provided a DNA construct which includes a DNA according to the fourth embodiment operatively linked to elements for the expression of said encoded protein.

10 According to a sixth embodiment of the invention, there is provided a transgenic plant harbouring a DNA construct according to the fifth embodiment.

According to a seventh embodiment of the invention, there is provided reproductive material of a transgenic plant according to the sixth embodiment.

15 According to an eighth embodiment of the invention, there is provided a composition comprising an antimicrobial protein according to the first embodiment together with an agriculturally-acceptable carrier diluent or excipient.

According to a ninth embodiment of the invention, there is provided a composition comprising an antimicrobial protein according to the first embodiment together with an pharmaceutically-acceptable carrier diluent or excipient.

20 According to a tenth embodiment of the invention, there is provided a method of controlling microbial infestation of a plant, the method comprising:

- i) treating said plant with an antimicrobial protein according to the first embodiment or a composition according to the eighth embodiment; or
- ii) introducing a DNA construct according to the fifth embodiment into said plant.

25 According to an eleventh embodiment of the invention, there is provided a method of controlling microbial infestation of a mammalian animal, the method comprising treating the animal with an antimicrobial protein according to the first embodiment or a composition according to the ninth embodiment.

30 According to a twelfth embodiment of the invention, there is provided a method of preparing an antimicrobial protein, which method comprises the steps of:

- a) obtaining or designing an amino acid sequence which forms a helix-turn-helix structure;
- b) replacing individual residues to achieve substantially the same distribution of positively charged residues and cysteine residues as in one or more of the amino acid sequences shown in Figure 4;

- c) synthesising a protein comprising said amino acid sequence chemically or by recombinant DNA techniques in liquid culture; and
- d) if necessary, forming disulphide linkages between said cysteine residues.

Other embodiments of the invention include methods for producing antimicrobial protein.

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BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 shows the results of cation-exchange chromatography of the basic protein fraction of a *Macadamia integrifolia* extract with the results of a bioassay for antimicrobial activity shown for fractions in the region of MiAMP2c elution.

Figure 2 shows the results of including 1 mM Ca^{2+} in a parallel bioassay of fractions from the cation-exchange separation.

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Figure 3 shows a reverse-phase HPLC profile of highly inhibitory fractions containing MiAMP2c from the cation-exchange separation in Figure 1 and 2 together with % growth inhibition exhibited by the HPLC fractions.

Figure 4 shows the amino acid sequences of MiAMP2a, b, c and d and protein fragments derived from other seed storage proteins which contain regions of homology to the MiAMP2 series of antimicrobial proteins.

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Figure 5 shows an example of a synthetic nucleotide sequence which can be used for the expression and secretion of MiAMP2c in transgenic plants.

Figure 6 shows the alignment of clones 1-3 from macadamia containing MiAMP2a, b, c and d subunits together with sequences from cocoa and cotton vicilin seed storage proteins which exhibit significant homology to the macadamia clones.

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Figure 7 displays a series of secondary structure predictions for MiAMP2c.

Figure 8 shows a three-dimensional model of the MiAMP2c protein.

Figure 9 shows stained SDS-PAGE gels of protein fractions at various stages in the expression and purification of TcAMP1 (Theobroma cacao subunit 1), MiAMP2a, MiAMP2b, MiAMP2c and MiAMP2d expressed in *E.coli* liquid culture.

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Figure 10 shows the reverse-phase HPLC purification of cocoa subunit 2 (TcAMP2) after the initial purification step using Ni-NTA media.

Figure 11 shows a western blot of crude protein extracts from various plant species using rabbit antiserum raised to MiAMP2c.

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Figure 12 shows a cation-exchange fractionation of the *Stenocarpus sinuatus* basic protein fraction along with the accompanying western blot which shows the presence of immunologically-related proteins in a range of fractions.

Figure 13 shows a reverse-phase HPLC separation of *Stenocarpus sinuatus* cation-exchange fractions which had previously reacted with MiAMP2c antibodies (see Figure 14). A western blot is also presented which reveals the presence of putative MiAMP2c homologues in individual HPLC fractions.

5 Figure 14 is a map of the binary vector pPCV91-MiAMP2c as an example of a vector that can be used to express these antimicrobial proteins in transgenic plants.

Figure 15 shows a western blot to detect MiAMP2c expressed in transgenic tobacco plants.

BEST MODE AND OTHER MODES FOR CARRYING OUT THE INVENTION

The following abbreviations are used hereafter:

10	EDTA	ethylenediaminetetraacetic acid
	IPTG	Isopropyl- β -D-thiogalactopyranoside
	MeCN	methyl cyanide (acetonitrile)
	Mi	<i>Macadamia integrifolia</i>
	MiAMP2	<i>Macadamia integrifolia</i> antimicrobial protein series number 2
15	Ni-NTA	Nickel-nitrilotriacetic acid chromatography media
	ND	not determined
	PCR	polymerase chain reaction
	PMSF	phenylmethylsulphonyl fluoride
	SDS-PAGE	sodium-dodecylsulphate polyacrylamide gel electrophoresis
20	TFA	trifluoroacetate

The term homologue is used herein to denote any polypeptide having substantial similarity in composition and sequence to the polypeptide used as the reference. The homologue of a reference polypeptide will contain key elements such as cysteine or other residues spaced at identical intervals such that a substantially similar three-dimensional global structure is adopted by the homologue as compared to the reference. The homologue will also exhibit substantially the same antimicrobial activity as the reference protein.

The present inventors have identified a new class of proteins with antimicrobial activity. Prototype proteins can be isolated from seeds of *Macadamia integrifolia*. The invention thus provides antimicrobial proteins *per se* and also DNA sequences encoding these antimicrobial proteins.

The invention also provides amino acid sequences of proteins which are homologous to the prototype antimicrobial proteins from *Macadamia integrifolia*. Thus, in addition to the antimicrobial proteins from Macadamia, this invention also provides amino acid sequences of homologues from other species which have hitherto been unrecognized as having antimicrobial activity.

While the first antimicrobial protein in the present series was isolated directly from *Macadamia integrifolia*, additional antimicrobial proteins were identified through cloning efforts, homology searches and subsequent antimicrobial testing of the encoded proteins after expression in and purification from liquid culture. After the first protein from this series was purified from macadamia and termed MiAMP2, clones were obtained which encoded a preproprotein containing MiAMP2. This large protein (666 amino acids), represented by several almost identical clones, contained four adjacent regions with significant similarity to the purified antimicrobial protein fragment (MiAMP2) which itself was found to lie within region three in the cloned nucleotide sequence; hence the purified antimicrobial protein is termed MiAMP2c. Other fragments contained in the 666-amino-acid clone are termed MiAMP2a, b and d as per their locations in the cloned nucleotide sequence. Several other sequences with significant homology to the MiAMP2a, b, c, and d protein fragments were then identified in the Entrez data base. These homologous sequences were contained within larger seed storage proteins from cotton and cocoa which sequences had not been previously described as containing antimicrobial protein sequences or as exhibiting antimicrobial activity. Fragments of larger seed storage proteins containing sequences homologous to MiAMP2c were tested and are here demonstrated to exhibit antimicrobial activity. Thus, the inventors have established a process for obtaining antimicrobial protein fragments from larger seed storage proteins. In the light of these findings, it is evident that fragments of other seed storage proteins containing sequences similar to the proteins described will also exhibit antimicrobial activity.

In particular, the 47-amino-acid TcAMP1 (for *Theobroma cacao* antimicrobial protein 1) and the 60-amino-acid TcAMP2 sequences were derived from a cocoa vicilin seed storage protein gene sequence (which contains 525 amino acids) (Spencer, M.E. and Hodge R. [1992] *Planta* 186:567-576). These derived fragments were then expressed in liquid culture. Cocoa vicilin fragments thus expressed and subsequently purified (Examples 10 and 11), were shown to be antimicrobial (Example 15). This is the first report that fragments of the cocoa vicilin protein possess antimicrobial activity. Pools of sequences containing fragments homologous to the MiAMP2c apparently released from cotton vicilin seed storage protein have been shown to possess antimicrobial activity (Chung, R. P.T. *et al.* [1997] *Plant Science* 127:1-16). This finding is clearly embodied in sequences disclosed in this application.

In addition to showing that cocoa-vicilin-derived fragments exhibit antimicrobial activity, there is herein described additional proteins which exhibit antimicrobial activity. For example, there is described below proteins from *Stenocarpus sinuatus* which are of similar size to MiAMP2 subunits, react with MiAMP2c antiserum, and contain sequences homologous to MiAMP2 proteins (see Figure 4). Based on the evidence provided herein, sequences homologous to the MiAMP2c

subunit (i.e., MiAMP2a, b, d; TcAMP1; TcAMP2; and cotton fragments 1, 2 and 3—see Figure 4) constitute proteins which contain the fragment with antimicrobial activity. The antimicrobial activity of MiAMP2 fragments from macadamia, and the TcAMP1 and 2 fragments from cocoa, is exemplified below. R. P. T. Chung *et al.* (*Plant Science* 127:1-16 [1997]) have demonstrated that the cotton fragments exhibit antimicrobial activity. Other antimicrobial proteins can also be derived from seed storage proteins such as peanut allergen Ara h (Burks, A.W. *et al.* [1995] *J. Clin. Invest.* 96 (4), 1715-1721), maize globulin (Belanger, F. C. and Kriz, A. L. [1991] *Genetics* 129 (3), 863-872), barley globulin (Heck, G. R. *et al.* [1993] *Mol. Gen. Genet.* 239 (1-2), 209-218), and soybean conglycinin (Sebastiani, F. L. *et al.* [1990] *Plant Mol. Biol.* 15 (1), 197-201), all of which contain the same key elements which are present in the sequences which are here shown to exhibit antimicrobial activity.

The proteins which contain regions of sequence homologous to MiAMP2 (as in Figure 4) can be used to construct nucleotide sequences encoding 1) the active fragments of larger proteins, or 2) fusions of multiple antimicrobial fragments. This can be done using standard codon tables and cloning methods as described in laboratory manuals such as *Current Protocols in Molecular Biology* (copyright 1987-1995 edited by Ausubel F. M. *et al.* and published by John Wiley & Sons, Inc., printed in the USA). Subsequently, these can be expressed in liquid culture for purification and testing, or the sequences can be expressed in transgenic plants after placing them in appropriate expression vectors.

The antimicrobial proteins *per se* will manifest a particular three-dimensional structure which may be determined using X-ray crystallography or nuclear magnetic resonance techniques. This structure will be responsible in large part for the antimicrobial activity of the protein. The sequence of the protein can also be subjected to structure prediction algorithms to assess whether any secondary structure elements are likely to be exhibited by the protein (see Example 8 and Figure 7). Secondary structures, thus predicted, can then be used to model three-dimensional global structures. Although three-dimensional structure prediction is not feasible for most proteins, the secondary structure predictions for MiAMP2c were sufficiently simple and clear that a three-dimensional model structure has been obtained for the MiAMP2c protein. Homologues exhibiting the same cysteine spacing and other key elements will also adopt the same three-dimensional structure. Example 8 shows that the structure most likely to be adopted by MiAMP2c (and homologues) is a helix-turn-helix structure stabilised by at least two disulfide bridges connecting the two antiparallel α -helical segments (see Figure 8). Additional stabilisation can be provided by an extra disulfide bridge (e.g., as in MiAMP2b) or by a hydrophobic ring-stacking interaction between tyrosine and/or phenylalanine residues (e.g., MiAMP2a and MiAMP2c), each located on the same face of the α -

helical segments as the normally present cysteine residues which participate in the 2 disulfide linkages mentioned above. NMR signals exhibited by MiAMP2c are consistent with the three-dimensional global model produced from the secondary-structure predictions mentioned above.

It will be appreciated that one skilled in the art could take a protein with known structure, alter the sequence significantly, and yet retain the overall three-dimensional shape and antimicrobial activity of the protein. One aspect of the structure that most likely could not be altered without seriously affecting the structure (and, therefore, the activity of the protein) is the content and spacing of the cysteine residues since this would disrupt the formation of disulfide bonds which are critical to a) maintaining the overall structure of the protein and/or b) making the protein more resistant to denaturation and proteolysis (stabilizing the protein structure). In particular, it is essential that cysteine residues reside on one face of the helix in which they are contained. This can best be accomplished by maintaining a three-residue spacing between the cysteine residues within each helix, but, can also be accomplished with a two-residue interval between the cysteine residues - provided the cysteines on the other helical segment are separated by three residues (i.e., C-X-X-C-X-X-X-C-nX-C-X-X-X-C-X-X-X-C where C is cysteine, X is any amino acid, and n is the number of residues forming a turn between the two α -helical segments). Aromatic tyrosine (or phenylalanine) residues can also function to add stability to the protein structure if they are located on the same face of the helix as the cysteine side chains. This can be accomplished by providing appropriate spacing of two or three residues between the aromatic residue and the proximate cysteine residue (i.e., Z-X-X-C-X-X-X-C-nX-C-X-X-X-C-X-X-X-Z where Z is tyrosine or phenylalanine).

The distribution of positive (and negative) charges on the various surfaces of the protein will also serve a critical role in determining the structure and activity of the protein. In particular, the distribution of positively-charged residues in an α -helical region of a protein can result in positive charges lying on one face of the helix or may result in the charged residues being concentrated in some particular portion of the molecule. An alternative distribution of positively charged residues is for them to project into the solvent in a radial orientation to the core of the protein. This orientation is predicted for several of the MiAMP2 homologues (data not shown). The spacing which is required for positioning of the residues on one face of the helix or the spacing required to accomplish a radial orientation from the core can easily be determined by one skilled in the art using a helical wheel plot with the sequence of interest. A helical wheel plot uses the fact that, in α -helices, each turn of the helix is composed of 3.6 residues on average. This number translates to 100° of rotational translation per residue making it possible to construct a plot showing the distribution of side chains in a helical region. Figure 8 shows how the spacing of charged residues can lead to most of the

positively charged side chains being localised on one face of the helix. It will be appreciated by one of skill in the art that positive charges are conferred by arginine and lysine residues.

In order for the protein to develop into a helix-turn-helix structure, it is also necessary to have particular residues that favor α -helix formation and that also favor a turn structure in the middle portion of the amino acid sequence (and disfavor a helical structure in the turn region). This can be accomplished by a proline residue or residues in the middle of the turn segment as seen with many of the MiAMP2 homologues. When proline is not present, glycine can also contribute to breaking a continuous helix structure, and inducing the formation of a turn at this position. In one case (i.e., TcAMP1), it appears that serine may be taking on this role. It will be appreciated that the residues in this region of the protein will usually favor the formation of a turn structure; residues which fulfill this requirement include proline, glycine, serine, and aspartic acid; but, other residues are also allowed.

The DNA sequences reported here are an extremely powerful tool which can be used to obtain homologous genes from other species. Using the DNA sequences, one skilled in the art can design and synthesise oligonucleotide probes which can be used to screen cDNA libraries from other species of plants for the presence of genes encoding antimicrobial proteins homologous to the ones described here. This would simply involve construction of a cDNA library and subsequent screening of the library using as the oligonucleotide probe one or part of one of the sequences reported here (such as sequence ID. No. 2 or the PCR fragment described in Example 9). Other oligonucleotide sequences coding for proteins homologous to MiAMP2 can also be used for this purpose (e.g., DNA sequences corresponding to cotton and cocoa vicilins). Making and screening of a cDNA library can be carried out by purchasing a kit for said purpose (e.g., from Stratagene) or by following well established protocols described in available DNA cloning manuals (see *Current Protocols in Molecular Biology, supra*). It is relatively straight forward to construct libraries of various species and to specifically isolate vicilin homologues which are similar to the Macadamia, cotton, or cocoa vicilins by using a simple DNA hybridization technique to screen such libraries. Once cloned, these vicilin-related sequences can then be examined for the presence of MiAMP2-like subunits. Such subunits can easily be expressed in *E. coli* using the system described in Examples 10 and 11. Subsequently, these proteins can also be expressed in transgenic.

Genes, or fragments thereof, under the control of a constitutive or inducible promoter, can then be cloned into a biological system which allows expression of the protein encoded thereby. Transformation methods allowing for the protein to be expressed in a variety of systems are known. The protein can thus be expressed in any suitable system for the purpose of producing the protein for further use. Suitable hosts for the expression of the protein include *E. coli*, fungal cells, insect cells,

mammalian cells, and plants. Standard methods for expressing proteins in such hosts are described in a variety of texts including section 16 (Protein Expression) of *Current Protocols in Molecular Biology* (*supra*).

Plant cells can be transformed with DNA constructs of the invention according to a variety of known methods (*Agrobacterium*, Ti plasmids, electroporation, micro-injections, micro-projectile gun, and the like). DNA sequences encoding the *Macadamia integrifolia* antimicrobial protein subunits (i.e. fragments a, b, c, or d from the MiAMP2 clones) as well as DNA coding for other homologues can be used in conjunction with a DNA sequence encoding a preprotein from which the mature protein is produced. This preprotein can contain a native or synthetic signal peptide sequence which will target the protein to a particular cell compartment (e.g., the apoplast or the vacuole). These coding sequences can be ligated to a plant promoter sequence that will ensure strong expression in plant cells. This promoter sequence might ensure strong constitutive expression of the protein in most or all plant cells, it may be a promoter which ensures expression in specific tissues or cells that are susceptible to microbial infection and it may also be a promoter which ensures strong induction of expression during the infection process. These types of gene cassettes will also include a transcription termination and polyadenylation sequence 3' of the antimicrobial protein coding region to ensure efficient production and stabilisation of the mRNA encoding the antimicrobial proteins. It is possible that efficient expression of the antimicrobial proteins disclosed herein might be facilitated by inclusion of their individual DNA sequences into a sequence encoding a much larger protein which is processed *in planta* to produce one or more active MiAMP2-like fragments.

Gene cassettes encoding the MiAMP2 series antimicrobial proteins (i.e., MiAMP2a, b, c, or d; or all of the subunits together; or the entire MiAMP2 clone) or homologues of the MiAMP2 proteins as described above can then be expressed in plant cells using two common methods. Firstly, the gene cassettes can be ligated into binary vectors carrying: i) left and right border sequences that flank the T-DNA of the *Agrobacterium tumefaciens* Ti plasmid; ii) a suitable selectable marker gene for the selection of antibiotic resistant plant cells; iii) origins of replication that function in either *A. tumefaciens* or *Escherichia coli*; and iv) antibiotic resistance genes that allow selection of plasmid-carrying cells of *A. tumefaciens* and *E. coli*. This binary vector carrying the chimaeric MiAMP2 encoding gene can be introduced by either electroporation or triparental mating into *A. tumefaciens* strains carrying disarmed Ti plasmids such as strains LBA4404, GV3101, and AGL1 or into *A. rhizogenes* strains such as A4 or NCCP1885. These *Agrobacterium* strains can then be co-cultivated with suitable plant explants or intact plant tissue and the transformed plant cells and/or regenerants selected using antibiotic resistance.

A second method of gene transfer to plants can be achieved by direct insertion of the gene in target plant cells. For example, an MiAMP2-encoding gene cassette can be co-precipitated onto gold or tungsten particles along with a plasmid encoding a chimaeric gene for antibiotic resistance in plants. The tungsten particles can be accelerated using a fast flow of helium gas and the particles
5 allowed to bombard a suitable plant tissue. This can be an embryogenic cell culture, a plant explant, a callus tissue or cell suspension or an intact meristem. Plants can be recovered using the antibiotic resistance gene for selection and antibodies used to detect plant cells expressing the MiAMP2 proteins or related fragments.

The expression of MiAMP2 proteins in the transgenic plants can be detected using either
10 antibodies raised to the protein(s) or using antimicrobial bioassays. These and other related methods for the expression of MiAMP2 proteins or fragments thereof in plants are described in *Plant Molecular Biology* (2nd ed., edited by Gelvin, S.B. and Schilperoort, R.A., © 1994, published by Kluwer Academic Publishers, Dordrecht, The Netherlands)

Both monocotyledonous and dicotyledonous plants can be transformed and regenerated.
15 Examples of genetically modified plants include maize, banana, peanut, field peas, sunflower, tomato, canola, tobacco, wheat, barley, oats, potato, soybeans, cotton, carnations, roses, sorghum. These, as well as other agricultural plants can be transformed with the antimicrobial genes such that they would exhibit a greater degree of resistance to pathogen attack. Alternatively, the proteins can be used for the control of diseases by topological application.

20 The invention also relates to application of antimicrobial protein in the control of pathogens of mammals, including humans. The protein can be used either in topological or intravenous applications for the control of microbial infections.

As indicated above in the description of the tenth embodiment, the invention includes within its scope the preparation of antimicrobial proteins based on the prototype MiAMP2 series of
25 proteins. New sequences can be designed from the MiAMP2 amino acid sequences which substantially retain the distribution of positively charged residues relative to cysteine residues as found in the MiAMP2 proteins. The new sequence can be synthesised or expressed from a gene encoding the sequence in an appropriate host cell. Suitable methods for such procedures have been described above. Expression of the new protein in a genetically engineered cell will typically result
30 in a product having a correct three-dimensional structure, including correctly formed disulphide linkages between cysteine residues. However, even if the protein is chemically synthesised, methods are known in the art for further processing of the protein to break undesirable disulfide bridges and form the bridges between the desired cysteine residues to give the desired three-dimensional structure should this be necessary.

Macadamia integrifolia antimicrobial proteins series number 2

As indicated above, a new series of potent antimicrobial proteins has been identified in the seeds of *Macadamia integrifolia*. The proteins collectively are called the MiAMP2 series of antimicrobial proteins (or MiAMP2 proteins) because they are all found on one large preproprotein which is processed into smaller subunits, each exhibiting antimicrobial activity; they represent the second class of antimicrobial proteins isolated from *Macadamia integrifolia*. Each protein fragment of the series has a characteristic pI value. MiAMP2a, b, c, and d subunits as shown in Figure 4 have predicted pI values of 4.4, 4.6, 11.5, and 11.6 respectively (predicted using raw sequence data without the His tag or cleavage sequences associated with expression of fragments in the vector pET16b), and contain two sets of CXXXC motifs which are important in stabilising the three-dimensional structure of the protein through the formation of disulfide bonds. Additionally, the proteins contain either an added set of aromatic (tyrosine/phenylalanine) residues or an added set of cysteine residues located at positions which would give more stability to the helix-turn-helix structure as described above and in Example 8.

The amino acid sequences of the MiAMP2 series of proteins share significant homology with fragments of previously described proteins in sequence databases (Swiss Prot and Non-redundant databases) searched using the BLASTP algorithm (Altschul, S.F. et al. [1990] *J. Mol. Biol.* 215:403). In particular, MiAMP2a, b, c and d sequences exhibit significant similarity with regions of cocoa vicilin and cotton vicilin (as seen in Figure 6). Some similarity is also seen with fragments from other seed storage proteins of peanut (Burks, A. W. et al. [1995] *J. Clin. Invest.* 96 (4), 1715-1721), maize (Belanger, F. C. and Kriz, A. L. [1991] *Genetics* 129 (3), 863-872), barley (Heck, G. R. et al. [1993] *Mol. Gen. Genet.* 239 (1-2), 209-218), and soybean (Sebastiani, F. L. et al. [1990] *Plant Mol. Biol.* 15 (1), 197-201). Although, in some cases the homology is not extremely high (for example, 18% identity between MiAMP2a and cotton subunit 1; see Figure 4), the spacing of the main four cysteine residues is conserved in all subunits and homologues. In addition, both cotton and cocoa vicilin-derived subunits retain the conserved tyrosine or phenylalanine residues as additional stabilisers of the tertiary structure. The cotton and cocoa vicilins with 525 and 590 amino acids, respectively, are much larger proteins than MiAMP2c (47 amino acids) (see Figures 4 and 6). Although MiAMP2 subunits also share some homology with MBP-1 antimicrobial protein from maize (Duvick, J.P. et al. (1992) *J Biol Chem* 267:18814-20) the number of residues between the CXXXC motifs is 13 which puts MBP-1 outside the specifications for the spacing given here in this application. MBP-1 is also a smaller protein (33 amino acids), overall, than the sequences claimed here and there is no evidence available the MBP-1 is derived from a larger seed storage protein other than some similarity with a portion of maize globulin protein. However, MBP-1 cannot be derived

from from the maize globulin since maize globulin contains 10 residues between the two CXXXXC motifs while MBP-1 contains 13. The alignments in Figures 4 and 6 show the similarity in cysteine spacing between MiAMP2 subunits and the cocoa and cotton vicilin-derived molecules. The cysteine and the aromatic tyrosine/phenylalanine residues in Figures 4 and 6 are highlighted with bold underlined text. Figure 4 also shows the alignment of additional proteins which can be expressed in liquid culture and shown to exhibit antimicrobial activity.

All of the MiAMP2 homologues that have been tested exhibit antifungal activity. MiAMP2 homologues show very significant inhibition of fungal growth at concentrations as low as 2 µg/ml for some of the pathogens/microbes against which the proteins were tested. Thus they can be used to provide protection against several plant diseases. MiAMP2 homologues can be used as fungicides or antibiotics by application to plant parts. The proteins can also be used to inhibit growth of pathogens by expressing them in transgenic plants. The proteins can also be used for the control of human pathogens by topical application or intravenous injection. One characteristic of the proteins is that inhibition of some microbes is suppressed by the presence of Ca^{2+} (1 mM). An example of this effect is provided for MiAMP2c subunit in Table 1.

Some of the MiAMP2 proteins and homologues could also function as insect control agents. Since some of the proteins are extremely basic (e.g., pI > 11.5 for MiAMP2c and d subunits), they would maintain a strong net-positive charge even in the highly alkaline environment of an insect gut. This strong net-positive charge would enable it to interact with negatively charged structures within the gut. This interaction may lead to inefficient feeding, slowing of growth, and possibly death of the insect pest.

Non-limiting examples of the invention follow.

Example 1

Extraction of Basic Protein from *Macadamia integrifolia* Seeds

Twenty five kilograms of Mi nuts (purchased from the Macadamia Nut Factory, Queensland, Australia) were ground in a food processor (The Big Oscar, Sunbeam) and the resulting meal was extracted for 2-4 hours at 4°C with 50 L of an ice-cold extraction buffer containing 10 mM NaH_2PO_4 , 15 mM Na_2HPO_4 , 100 mM KCl, 2 mM EDTA, 0.75% polyvinylpolypyrrolidone, and 0.5 mM phenylmethylsulfonyl fluoride (PMSF). The resulting homogenate was run through a kitchen strainer to remove larger particulate material and then further clarified by centrifugation (4000 rpm for 15 min) in a large capacity centrifuge. Solid ammonium sulphate was added to the supernatant to obtain 30% relative saturation and the precipitate allowed to form overnight with stirring at 4°C. Following centrifugation at 4000 rpm for 30 min, the supernatant was taken and ammonium sulphate added to achieve 70% relative saturation. The solution was allowed to precipitate overnight and then

centrifuged at 4000 rpm for 30 min in order to collect the precipitated protein fraction. The precipitated protein was resuspended in a minimal volume of extraction buffer and centrifuged once again (13,000 rpm x 30 min) to remove the any insoluble material yet remaining. After dialysis (10 mM ethanolamine pH 9.0, 2 mM EDTA and 1 mM PMSF) to remove residual ammonium sulphate, the protein solution was passed through a Q-Sepharose Fast Flow column (5 x 12 cm) previously equilibrated with 10 mM ethanolamine (pH 9), 2 mM in EDTA). The collected flowthrough from this column represents the basic (pI >9) protein fraction of the seeds. This fraction was further purified as described in Example 3.

Example 2

Antifungal and Antibacterial Activity Assays

In general, bioassays to assess antifungal and antibacterial activity were carried out in 96-well microtitre plates. Typically, the test organism was suspended in a synthetic growth medium consisting of K₂HPO₄ (2.5 mM), MgSO₄ (50 µM), CaCl₂ (50 µM), FeSO₄ (5 µM), CoCl₂ (0.1 µM), CuSO₄ (0.1 µM), Na₂MoO₄ (2 µM), H₃BO₃ (0.5 µM), KI (0.1 µM), ZnSO₄ (0.5 µM), MnSO₄ (0.1 µM), glucose (10 g/L), asparagine (1 g/L), methionine (20 mg/L), myo-inositol (2 mg/L), biotin (0.2 mg/L), thiamine-HCl (1 mg/L) and pyridoxine-HCL (0.2 mg/L). The test organism consisted of bacterial cells, fungal spores (50,000 spores/ml) or fungal mycelial fragments (produced by blending a hyphal mass from a culture of the fungus to be tested and then filtering through a fine mesh to remove larger hyphal masses). Fifty microlitres of the test organism suspended in medium was placed into each well of the microtitre plate. A further 50 µl of the test antimicrobial solution was added to appropriate wells. To deal with well-to-well variability in the bioassay, 4 replicates of each test solution were done. Sixteen wells from each 96-well plate were used as controls for comparison with the test solutions.

Unless otherwise stated, incubation was at 25°C for 48 hours. All fungi including yeast were grown at 25°C. *E. coli* were grown at 37°C and other bacteria were bioassayed at 28°C. Percent growth inhibition was measured by following the absorbance at 600 nm of growing cultures over various time intervals and is defined as 100 times the ratio of the average change in absorbance in the control wells minus the change in absorbance in the test well divided by the average change in absorbance at 600 nm for the control wells (i.e., [(avg change in control wells - change in test well) / (avg change in control wells)] x 100). Typically, measurements were taken at 24 hour intervals and the period from 24-48 hours was used for %Inhibition measurements.

Example 3

Purification of antimicrobial protein from *Macadamia integrifolia* basic protein fraction

The starting material for the isolation of the Mi antimicrobial protein was the basic fraction extracted from the mature seeds as described above in Example 1. This protein was further purified
5 by cation exchange chromatography as shown in Figure 1.

About 4 g of the basic protein fraction dissolved in 20 mM sodium succinate (pH 4) was applied to an S-Sepharose High Performance column (5 X 60 cm) (Pharmacia) previously equilibrated with the succinate buffer. The column was eluted at 17 ml/min with a linear gradient of 20 L from 0 to 2 M NaCl in 20 mM sodium succinate (pH 4). The eluate was monitored for protein
10 by on-line measurement of the absorbance at 280 nm and collected in 200 ml fractions. Portions of each fraction were subsequently tested in the antifungal activity assay against *Phytophthora cryptogea* at a concentration of 100 µg/ml in the presence and absence of 1 mM Ca^{2+} . Results of bioassays are included in Figures 1a and 1b where the elution gradient is shown as a solid line and the shaded bars represent %Inhibition. The Figure 1a assays were conducted without added Ca^{2+} while 1 mM Ca^{2+}
15 was included in the Figure 1b assays. Fractionation yielded a number of unresolved peaks eluting between 0.05 and 2 M NaCl. A peak eluting at about 16 hours into the separation (fractions 90-92) showed significant antimicrobial activity.

Fractions showing significant antimicrobial activity were further purified by reversed-phase chromatography. Aliquots of fractions 90-92 were loaded onto a Pep-S (C_2/C_{18}), column (25 x 0.93
20 cm) (Pharmacia) equilibrated with 95% $\text{H}_2\text{O}/5\%$ MeCN/0.1% TFA (=100%A). The column was eluted at 3 ml/min with a 240 ml linear gradient (80 min) from 100%A to 100%B (=5% $\text{H}_2\text{O}/95\%$ MeCN/0.1% TFA). Individual peaks were collected, vacuum dried three times in order to remove traces of TFA, and subsequently resuspended in 500 microlitres of milli-Q water (Millipore Corporation water purification system) for use in bioassays as described in Example 2. Figure 2
25 shows the HPLC profile of purified fraction 92 from the cation-exchange separation shown in Figures 1 and 2. Protein elution was monitored at 214 nm. The acetonitrile gradient is shown by the straight line. Individual peaks were bioassayed for antimicrobial activity: the bars in Figure 3 show the inhibition corresponding to 15 µg/ml of material from each of the fractions. The active protein elutes at approximately 27 min (~30% MeCN/0.1%TFA) and is called MiAMP2c.

30

Example 4

Purity of Isolated MiAMP2c

The purity of the isolated antimicrobial protein was verified by native SDS-PAGE followed by staining with coomassie blue protein staining solution. Electrophoresis was performed on a 10-20% tricine gradient gel (Novex) as per the manufacturers recommendations (100 V, 1-2 hour separation

time). Under these conditions the purified MiAMP2c migrates as a single discrete band (<10 kDa in size). The detection of a single major band in the SDS-PAGE analysis together with single peaks eluting in the cation-exchange and reversed-phase separations (not shown), gives strong indication that the MiAMP2c preparation is greater than 95% pure and therefore the activity of the preparation was almost certainly due to the MiAMP2c alone and not to a minor contaminating component. A clean signal in mass spectrometric analysis (Example 5 below) also supports this conclusion.

Example 5

Mass Spectroscopic Analysis of MiAMP2c

Purified MiAMP2c was submitted for mass spectroscopic analysis. Approximately 1 µg of protein in solution was used for testing. Analysis showed the protein to have a molecular weight of 6216.8 Da ± 2 Da. Additionally, the protein was subjected to reduction of disulfide bonds with dithiothreitol and alkylation with 4-vinylpyridine. The product of this reduction/alkylation was then submitted for mass spectroscopic analysis and was shown to have gained 427 mass units (i.e. molecular weight was increased by approximately 4 X 106 Da). The gain in mass indicated that four 4-vinylpyridine groups had reacted with the reduced protein, demonstrating that the protein contains a total of 4 cysteine residues. The cysteine content has also been subsequently confirmed through amino acid sequencing.

Example 6

Amino Acid Sequence of MiAMP2c Protein

Approximately 1 µg of the pure protein which had been reduced and alkylated was subjected to Automated Edman degradation N-terminal sequencing. In the first sequencing run, the sequence of the first 39 residues was determined. Subsequently, approximately 1 mg of MiAMP2c was reacted with Cyanogen Bromide which cleaved the protein on the C-terminal side of Methionine-26. The C-terminal fragment generated by the cleavage reaction was purified by reversed-phase HPLC and sequenced, yielding the remaining sequence of MiAMP2c (i.e. residues 27-47). The full amino acid sequence is RQRDP QQQYE QCQER CQRHE TEPRH MQTCQ QRCER RYEKE KRKQQ KR and represents amino acids 118 to 164 of clone 3 from Example 9 (see Figure 6 and SEQUENCE ID NO: 5). In the figure, cysteine residues are in bold type and underlined to facilitate recognition of the spacing patterns. Depending on the number of disulfide bonds that are formed, the protein mass will range from 6215.6 to 6219.6 Da. This is in close agreement with the mass of 6216.8 ± 2 Da obtained by mass spectrometric analysis (Example 5). The measured mass closely approximates the predicted mass of MiAMP2c in a two-disulfide form as is expected to be the case.

Example 7

Synthetic DNA Sequence Coding for MiAMP2c with a leader peptide

Using standard codon tables it is possible to reverse-translate the protein sequences to obtain DNA sequences that will code for the antimicrobial proteins. The software program MacVector 4.5.3 was used to enter the protein sequence and obtain a degenerate nucleotide sequence. A codon usage table for tobacco was referenced in order to pick codons that would be adequately represented in tobacco for purposes of obtaining high expression in this test plant. A 30 amino-acid leader peptide was also designed to ensure efficient processing of the signal peptide and secretion of the peptide extracellularly. For this purpose, the method of Von Hiejne was used to evaluate a series of possible leader sequences for probability of cleavage at the correct position [Von Hiejne, G.(1986) *Nucleic Acids Research* 14(11): 4683-4690]. In particular, the amino acid sequence MAWFH VSVCN AVFVV IIIIM LLMFV PVVRG (Sequence ID. No. 11) was found to give an optimal probability of correct processing of the signal peptide immediately following the G (Gly) of this leader sequence. A 5' untranslated region from tobacco mosaic virus was also added to this synthetic gene to promote higher translational efficiency [Dowson, M.J., *et al.* (1994) *Plant Mol. Biol. Rep.* 12(4):347-357]. The synthetic gene also contains restriction sites at the 5' and 3' ends and immediately 5' of the start ATG for efficient cloning and subcloning procedures. Figure 5 shows a synthetic DNA sequence suitable for use in plant expression experiments. In this Figure, the arrow shows where translation is initiated and the triangular symbol indicates the point of cleavage of the signal peptide.

Example 8

Structure prediction of MiAMP2c Protein

Using sequence analysis algorithms, putative secondary structure motifs can be assigned to the protein. Five different algorithms were used to predict whether α -helices, β -sheets, or turns can occur in the MiAMP2c protein (Figure 4). Methods were obtained from the following sources: DPM method, Deleage, G., and Roux, B. (1987) *Prot. Eng.* 1:289-294; SOPMA method, Geourjon, C., and Deleage, G. (1994) *Prot. Eng.* 7:157-164; Gibrat method, Gibrat, J.F., Garnier, J., and Robson, B.(1987) *J.Mol.Biol.* 198:425-443; Levin method, Levin, J.M., Robson, B., and Garnier, J. (1986) *FEBS Lett.* 205:303-308; and PhD method, Rost, B., And Sander, C. (1994) *Proteins* 19:55-72. Figure 7 shows the predicted locations of α -helices, β -sheets and turns. The following symbols have been used in Figure 7: C, coil (unstructured); H, alpha helix; E, β - sheet; and S, turn. Underlined residues are those which were predicted to exhibit an α -helical structure by at least 2 separate structure prediction methods; these are represented as helices in Figure 8.

It is clear from the secondary structure predictions that the protein is highly α -helical. While secondary structure prediction is often difficult and inaccurate, this particular prediction gives a clear indication of the structure of the protein. Examination of the secondary-structure predictions show a clear preponderance of two α -helical regions broken by a stretch of about 5-8 residues. This is highly suggestive of a helix-turn-helix motif.

Helical wheel analysis of the MiAMP2c amino acid sequence shows that cysteine residues with a CXXXC spacing will be aligned on one face of the helix in which they are located. Since the cysteines are involved in disulfide bond formation, the cysteine side chains in one helix must form covalent bonds with the cysteine side chains located on the other helical segment. When the helical segments are arranged in such a way as to bring the cysteine side chains from each respective helix into proximity with the other cysteine side chains, the resulting three-dimensional structure is shown in Figure 8. This structure exhibits a remarkable distribution of positively charged residues on one face of the protein comprised of two helices held together by two disulfide bonds. Figure 8 shows how the spacing of positively charged residues in helical regions of this molecule will cause these side chains to lie on one face of the helix. The positively charged residues are the dark side chains outlined in black. Other dark side chains represent acidic residues. A proline residue (grey colour marked with a 'P') is located at the extreme left end of the molecule in the turn region. Solid black lines show where disulfide bonds connect the two helices. The dotted line shows where the two aromatic hydrophobic residues interact to add stability to the helix-turn-helix structure.

This helix-turn-helix structure will be adopted by all MiAMP2 homologues containing the same cysteine spacing and residues with helix and turn-forming propensities. Other MiAMP2 fragment sequences can be superimposed onto the global structure shown in figure 8. The overall structure will remain essentially the same but the charge distribution will vary according to the sequences involved. In the case of MiAMP2b, the dotted line would represent an added disulfide bridge instead of a hydrophobic interaction.

Example 9

cDNA cloning of genes corresponding to MiAMP2c

PCR Amplification of a genomic fragment of the MiAMP2c gene

Using the reverse-translated nucleotide sequences, degenerate primers were made for use in PCR reactions with genomic DNA from Macadamia. Primer JPM17 sequence was 5' CAG CAG CAG TAT GAG CAG TG 3' and primer JPM20 degenerate sequence was 5' TTT TTC GTA (T/T)C(T/G) (G/T)C(T/G) TTC GCA 3' (SEQ ID NOS: 12 and 13). Primers JPM17 and JPM20 were used in PCR amplifications carried out for 30 cycles with 30 sec at 95°C, 1 min at 50°C, and 1 min at 72°C. PCR products with sizes close to those which were expected were directly sequenced

(ABI PRISM Dye Terminator Cycle Sequencing Ready Reaction Kit from Perkin Elmer Corporation) after excising DNA bands from agarose gels and purifying them using a Qiagen DNA clean-up kit. Using this approach, it was possible to amplify a fragment of DNA of approximately 100 bp. Direct sequencing of this nucleotide fragment yielded the nucleotide sequence
5 corresponding to a portion of the amino acid sequence of the antimicrobial protein MiAMP2c (amino acids 7-39 of Figure 4). The partial nucleotide sequence obtained from the above-mentioned fragment excluding the primer sequences was 5' TCA GAA GCG CTG CCA ACG GCG CGA GAC AGA GCC ACG ACA CAT GCA AAT TTG TCA ACA ACG C 3' (corresponding to base pairs 264 to 324 in SEQ ID NO: 6). This sequence can be used for a variety of purposes including screening of
10 cDNA and genomic libraries for clones of MiAMP2 homologues or design of specific primers for PCR amplification reactions.

Messenger RNA isolation from Macadamia nut kernels

Fifty-eight grams of Macadamia nut kernels were ground to powder under liquid nitrogen using a mortar and pestle. RNA from ground material was then purified using a Guanidine
15 thiocyanate/Cesium chloride technique (*Current Protocols in Molecular Biology, supra*). Using this method approximately 5 mg of total RNA was isolated. Messenger RNA was then purified from total RNA using a spun column mRNA purification kit (Pharmacia).

cDNA library construction

A cDNA library was constructed in a lambda ZAP vector using a library kit from Stratagene.
20 A total of 6 reactions were performed using 25 micrograms of messenger RNA. First and second strand cDNA synthesis was performed using MMLV Reverse transcriptase and DNA Polymerase I, respectively. After blunting the cDNA with *Pfu* DNA Polymerase, *Eco* RI linker adapters were ligated to the DNA. DNA was then kinased using T4 polynucleotide kinase and the DNA subsequently digested with *Xho* I restriction endonuclease. At this point cDNA material was
25 fractionated according to size using a sephacryl-S500 column supplied with the kit. DNA was then ligated into the lambda ZAP vector. The vector containing ligated insert was then packaged into lambda phage (Gigapack III packaging extract from Stratagene).

Screening of library

The library constructed above was then plated and screened in XL1-blue *E. coli* bacterial lawns
30 growing in top agarose. Plaques containing individual clones were isolated by lifting onto Hybond N+ membranes (Amersham LIFE SCIENCE), hybridizing to a radiolabeled version of the genomic DNA fragment amplified above, imaging of the blot, and picking of possitive clones for the next round of screeing. After secondary and tertiary screening, plaques were sufficiently isolated to allow

picking of single clones. Several clones were obtained, and subsequently the pBK-CMV vector portion from the larger lambda vector was excised.

Sequence of MiAMP2c cDNA clones

Vectors (pBK-CMV) containing putative MiAMP2c clones were sequenced to obtain the DNA
 5 sequence of the cloned inserts. Seven clones were partially sequenced and an additional three clones were fully sequenced (see SEQ ID NOS: 2, 4 and 6 for DNA sequences of the macadamia clones). Translation of the DNA sequences showed that the full length clones encoded highly similar proteins of 666 amino acids. Figure 6 shows that these proteins have substantial similarity to vicilin seed-storage proteins from cocoa and cotton. Stars show positions of conserved identities and dots show
 10 positions of conserved similarities. Examination of the protein sequences revealed that the exact MiAMP2c sequence is found within the translated protein sequence of clone 3 at amino acid positions 118 to 164 (see Figure 6); clones 1 and 2 contained sequences differing from MiAMP2c by 2 residues and 3 residues, respectively, out of 47 amino acids total in the MiAMP2c sequence.

The translation products of the full-length clones (i.e., clones 1 and 2) consist of a short signal
 15 peptide from residues 1 to 28, a hydrophilic region from residues 29 to ~246, and then two segments stretching from residues ~246 to 666 with a stretch of acidic residues separating them at positions 542-546.

Significantly, the hydrophilic region containing the sequence for MiAMP2c, also contains 3 additional segments which are very similar to MiAMP2 (termed MiAMP2a, b and d). These 4
 20 segments (found between residues 28 and ~246) are separated by stretches in which approximately four out of five residues are acidic (usually glutamic acid). These acidic stretches occur at positions 64-68, 111-115, 171-174, and 241-246 and appear to delineate processing sites for cleavage of the 666-residue preproprotein into smaller functional fragments (acidic stretches delineating cleavage sites are shown as bold characters in Figure 6). All four MiAMP2-like segments of the protein
 25 contain 2 doublets of cysteine residues separated by 10-12 residues to give the following pattern C-X-X-X-C-(10-12X)-C-X-X-X-C where X is any amino acid, and C is cysteine. All four segments are expected to form helix-turn-helix motifs as described in Example 8 above. It is clear that the cysteines in these locations will form disulfide bridges that stabilize the structure of the proteins by holding the two helical portions together.

30 The predicted helix-turn-helix motifs can be further stabilized in several ways. The first method of stabilization is exemplified in segments 1 and 3 (i.e., residues 29-63 and 118-170, respectively, of the 666-residue Macadamia vicilin-like protein). These segments are stabilized by a hydrophobic ring-stacking interaction between two aromatic residues (one on each α -helical segment); this is normally accomplished with tyrosine residues but phenylalanine is also

used. As with the cysteine residues, the location of these aromatic residues in the predicted α -helical segments is critical if they are to offer stabilization to the helix-turn-helix structure. In segments 1 and 3, the aromatic residues are 2 and 3 residues removed from the cysteine doublets as shown here: Z-X-X-C-X-X-X-C-(10-12X)-C-X-X-X-C-X-X-X-Z where C is cysteine and Z is usually tyrosine but can be substituted with phenylalanine as is done in segment 1.

The second way to stabilize the helix-turn-helix fragment is by using an added disulfide bridge as seen in fragment 2 (residues 71-110). This is accomplished by placing additional cysteine residues 2 and 3 residues removed from the cysteine doublets as shown here: nX-C-X-X-C-X-X-X-C-(10-12X)-C-X-X-X-C-X-X-X-C-nX. This is the only report that the inventors know of where a helix-turn-helix domain in an antimicrobial protein is stabilized by three disulfide bridges. While segment 4 (residues 175-241) does not contain the extra disulfide bridge or the hydrophobic ring-stacking stabilization, it is probably stabilized by means of weaker ionic and or hydrogen bonding interactions.

Example 10

Vectors for liquid culture expression of MiAMP2 and homologues

PCR primers flanking the nucleotide region coding for MiAMP2c were engineered to contain restriction sites for *Nde* I and *Bam* HI (corresponding to the 5' and 3' ends of the coding region, respectively; Primer JPM31 sequence: 5' A CAC CAT ATG CGA CAA CGT GAT CC 3'; Primer JPM32 sequence: 3' C GTT GTT TTC TCT ATT CCT AGG GTT G 5', SEQ ID NOS: 14 and 15). These primers were then used to amplify the coding region of MiAMP2c DNA. The PCR product from this amplification was then digested with *Nde* I and *Bam* HI and ligated into a pET17b vector (Novagen / Studier, F. W. *et al.* [1986] *J. Mol. Biol.* 189:113) with the coding region in-frame to produce the vector pET17-MiAMP2c.

A similar approach to the one above was used to construct vectors carrying the coding sequences of MiAMP2c homologues (i.e. MiAMP2a, b, and d as well as Tc AMP1, and TcAMP2). To construct the expression vectors for fragments a, b and d in MiAMP2 clone 1, specific PCR primers incorporating the *Nde* I and *Bam* HI sites were designed to amplify the fragments of interest. The products were then digested with the appropriate restriction enzymes and ligated into the *Nde* I/*Bam* HI sites of a pET16b vector [Novagen] containing a His tag and a Factor Xa cleavage site (amino acid sequence MGHHH HHHHH HHSSG HIEGR HM, SEQ ID NO: 16). The protein products expressed from the pET16b vector is a fusion to the antimicrobial protein. The coding sequences for MiAMP2-like subunits from cocoa (Figure 4, TcAMP1 and TcAMP2) were obtained from the published DNA sequence of the cocoa vicilin gene (Spencer, M. E. and Hodge R. [1992] *Planta* 186:567-576). Two MiAMP2-like fragments within the cocoa vicilin gene were located at

the 5' end (corresponding to the residues shown in Figure 4), and two sets of complimentary oligonucleotides corresponding to the desired coding sequences were designed. The complimentary oligonucleotides (90 to ~100 bases) corresponding to each cocoa subunit contained a 20bp overlap and also contained the *Nde* I and *Bam* HI restriction endonuclease cut sites.

5 For TcAMP, the following nucleotides were synthesised:

TcAMP1 forward oligo 5' GGGAATTCCA TATGTATGAG CGTGATCCTC
GACAGCAATA CGAGCAATGC CAGAGGCGAT
GCGAGTCGGA AGCGACTGAA GAAAGGGAGC 3';

10 TcAMP1 reverse oligo 5' GAAGCGACTG AAGAAAGGGA GCAAGAGCAG
TGTGAACAAC GCTGTGAAAG GGAGTACAAG
GAGCAGCAGA GACAGCAATA GGGATCCACA C 3'.

For TcAMP2, the following oligonucleotides were used:

15 TcAMP2 forward oligo 5' GGGAATTCCA TATGCTTCAA AGGCAATACC
AGCAATGTCA AGGGCGTTGT CAAGAGCAAC
AACAGGGGCA GAGAGAGCAG CAGCAGTGCC
AGAGAAAATG C 3';

20 TcAMP2 reverse oligo 5' GTGTGGATCC CTAGCTCCTA TTTTTTTTGT
GATTATGGTA ATTCTCGTGC TCGCCTCTCT
CTTGTTCCCTT ATATTGCTCC CAGCATTTTC
TCTGGCACTG CT 3'.

The oligonucleotide sets were added to individual PCR amplification reactions in order make individual PCR fragments containing the desired coding region. Since initial PCR amplifications gave fuzzy bands, reamplification of the original products was carried out using new 20mer primers (complimentary to the 5'ends of the forward and reverse oligonucleotides shown above) designed to
25 amplify the entire coding region of the cocoa subunits. Once amplified, the PCR products were restriction digested with the appropriate enzymes and ligated into the vector pET16b as above. This procedure was carried out for both cocoa fragments with similarities to MiAMP2c (shown in Figure 4).

Example 11

30 Expression in *E.coli* and purification of MiAMP2c and homologues

Starter cultures (50 ml) of *E.coli* strain BL21 (Grodberg, J. [1988] *J. Bacteriol.* 170:1245) transformed with the appropriate pET construct (Example 10) were added to 500ml of NZCYM media (*Current Protocols in Molecular Biology, supra*) and cultured to an optical density of 0.6 (600 nm) and induced with the addition of 0.4 or 1.0 mM IPTG depending on whether pET17b

(containing a T7 promoter) or pET16b (containing a His tag fusion and a T7 promoter/lac operator) vector was being used. After cells were induced, cultures were allowed to grow for 4 hours before harvesting. Aliquots of the growing cultures were removed at timed intervals and protein extracts run on an SDS-PAGE gel to follow the expression levels of MiAMP2 and homologues in the

5 cultures. Fragments being expressed with a Histidine tag (i.e., in the pET16b vector), were harvested by centrifuging induced cell cultures at 5000g for 10 minutes. Cell pellets were resuspended and broken by stirring for one hour in 6 M Guanidine-HCl, buffered with 100 mM sodium phosphate and 10 mM Tris at pH 8.0. Broken cell suspensions were centrifuged at 10,000g for 20-30 minutes to settle the cellular debris. Supernatants were removed to fresh tubes and 500 mg of Ni-NTA fast flow

10 resin (Qiagen) was added to each supernatant. After gentle mixing at 4°C for 30-60 minutes, the suspension was loaded into a small column, rinsed two times with 8 M Urea (pH 8.0 and then pH 6.3) and subsequently, the protein was eluted using 8 M Urea pH 4.5. Protein fractions thus obtained were substantially pure but were further purified using an 9.3 x 250 mm C2/C18 reverse phase column (Pharmacia) and 75 minute gradient from 5% to 50% acetonitrile (0.1% TFA) flowing at 3

15 ml/min (data not shown).

All of the MiAMP2c homologues (except MiAMP2c which was expressed in pET17b) were expressed in the pET16b vector containing the Histidine tag. While induction of the MiAMP2c culture proceeded as above, the rest of the purification was somewhat different. In this case, MiAMP2c-expressing cells were harvested by centrifugation but were then resuspended in phosphate

20 buffer (100 mM, pH 7.0 containing 10 mM EDTA and 1 mM PMSF) and broken open using a French press instrument. Cellular debris containing MiAMP2c inclusion bodies was solubilized using a 6 M Guanidine-HCl, 10 mM MES pH 6.0 buffer. Soluble material was then recovered after centrifugation to remove insoluble debris remaining from the solubilization step. Guanidine-HCl soluble material was then dialyzed against 10 mM MES pH 6.0 containing PMSF (1 mM) and EDTA

25 (10 mM). Cation-exchange fractionation was carried out as described in Example 3 except on a smaller scale after the dialysis step. Subsequently, the major eluting protein from the cation-exchange column, which was MiAMP2c, was then further purified using reverse phase HPLC as described in Example 3.

Figure 9 shows the SDS-PAGE gel analysis of the various purification stages obtained

30 following induction with IPTG and subsequent purification of expressed proteins. Samples analysed during the TcAMP1 purification were as follows: lane 1, molecular weight markers; lane 2, Ni-NTA non-binding fraction; lane 3, rinse of Ni-NTA resin with pH 8 urea; lane 4, rinse of Ni-NTA resin with pH 6.3 urea; lane 5, elution of TcAMP1 with pH 4.5 urea; and lane 6, second elution of TcAMP1 with pH 4.5 urea. TcAMP2 was purified in a similar manner and was also subjected to

reverse-phase HPLC to further purify the fraction eluting from the Ni-NTA resin. Figure 10 shows the reverse phase purification of cocoa subunit number 2 (TcAMP2).

SDS-PAGE gel analysis of the MiAMP2a, b, and d fragment purification is shown in the second panel of Figure 9. Lane contents are as follows: lane 1, molecular weight markers; lane 2, MiAMP2a pre-induced cellular extract; lane 3, MiAMP2a IPTG induced cellular extract; lane 4, MiAMP2a Ni-NTA non-binding fraction; lane 5, MiAMP2a elution from Ni-NTA; lane 6, MiAMP2b pre-induced cellular extract; lane 7, MiAMP2b IPTG induced cellular extract; lane 8, MiAMP2b Ni-NTA non-binding fraction; lane 9, MiAMP2b elution from Ni-NTA; lane 10, MiAMP2d pre-induced cellular extract; lane 11, MiAMP2d IPTG induced cellular extract; lane 12, MiAMP2d Ni-NTA non-binding fraction; and lane 13, MiAMP2d elution from Ni-NTA.

Using the vectors described in Example 10, MiAMP2c, and 5 homologues (i.e., MiAMP2a, MiAMP2b, MiAMP2d, TcAMP1 and TcAMP2) were all expressed, purified and tested for antimicrobial activity. The approach taken above can be applied to all of the antimicrobial fragments described in Figure 4. Purified fragments can then be tested for specific inhibition against microbial pathogens of interest.

Example 12

Detection of MiAMP2 homologues in other species using antibodies raised to MiAMP2c

Rabbits were immunised intramuscularly according to standard protocols with MiAMP2 conjugated to diphtheria toxoid suspended in Freund's incomplete adjuvant. Serum was harvested from the animals at regular intervals after giving the animal added doses of MiAMP2 adjuvant to boost the immune response. Approximately 100 ml of serum were collected and used for screening of crude extracts obtained from several plant seeds. One hundred gram quantities of seeds were ground and extracted to obtain a crude extract as in Example 1. Aliquots of protein were separated on SDS-PAGE gels and the gels were then blotted onto nitrocellulose membrane for subsequent detection of antibody reacting proteins. The membranes were incubated with MiAMP2c rabbit primary antibodies, washed and then incubated with alkaline phosphatase-conjugated goat anti-rabbit IgG for colorimetric detection of antigenic bands using the chemical 5-bromo-4-chloro-3-indolyl phosphate / nitroblue tetrazolium substrate system (Schleicher and Schuell). Figure 11 shows that various other species contain immunologically-related proteins of similar size to MiAMP2c. Lanes 1-15 contain the extracts from the following species: 1) *Stenocarpus sinuatus*, 2) *Stenocarpus sinuatus* (1/10 loading), 3) *Restio tremulus*, 4) *Mesomalaena tetragona*, 5) *Nitraria billardieri*, 6) *Petrophile canescens*, 7) *Synaphae acutiloba*, 8) *Dryandra formosa*, 9) *Lambertia inermis*, 10) *Stirlingia latifolia*, 11) *Xylomelum angustifolium*, 12) *Conospermum bracteosum*, 13) *Conospermum triplinernium*, 14) Molecular weight marker, 15) *Macacamia integrifolia* pure MiAMP2c. Lanes 1-

13 contain a variety of species, some of which show the presence of antigenically related proteins of a similar size to MiAMP2c. Other bands exhibiting higher molecular weights probably represent the larger precursor seed storage proteins from which the antimicrobial proteins are derived.

Antigenically-related proteins can be seen in lanes 1, 2, 4, 6, 7, 8, 9, and 11-13.

- 5 Bioassays were also performed using crude extracts from various Proteaceae species. Specifically, extracts from *Banksia robur*, *Banksia canei*, *Hakea gibbosa*, *Stenocarpus sinuatus*, and *Stirlingia latifolia* have all been shown to exhibit antimicrobial activity. This activity may derive from MiAMP2 homologues since these species are related to Macadamia.

Example 13

- 10 Purification of MiAMP2c homologues in another species using antibodies raised to MiAMP2c

Based on the detection of immunologically related proteins in other species of the family Proteaceae and the presence of antimicrobial activity in crude extracts, *Stenocarpus sinuatus* was chosen for a large scale fractionation experiment in an attempt to isolate MiAMP2c homologues. Five kg of *S.sinuatus* seed was frozen in liquid nitrogen and ground in a food processor (Big Oscaar
15 Sunbeam). The ground seed was immediately placed into 12 L of 50 mM H₂SO₄ extraction buffer and extracted at 4°C for 1 hour with stirring. The slurry was then centrifuged for 20 min at 10,000 g to remove particulate matter. The supernatant was then adjusted to pH 9 using a 50mM ammonia solution. PMSF and EDTA were added to final concentrations of 1 and 10 mM respectively.

- The crude protein extract was applied to an anion exchange column (Amberlite IRA-938,
20 Rohm and Haas) (3cmx90cm) equilibrated with 50 mM NH₄Ac pH 9.0 at a flow rate of 40 ml/min. The unbound protein comprising the basic protein fraction was collected and used in the subsequent purification steps.

- The basic protein fraction was adjusted to pH 5.5 with acetic acid and then applied at 10 ml/minute over 12 h to a SP-Sepharose Fast Flow (Pharmacia) Column (5cm x 60cm) pre-
25 equilibrated with 25mM ammonium acetate. The column was then washed for 3.5 h with 25 mM Acetate pH 5.5. Elution of bound proteins was achieved by applying a linear gradient of NH₄Ac from 25 mM to 2.0 M (pH 5.5) at 10 ml/min over 10 h. Absorbance of the eluate was observed at 280 nm and 100 ml fractions collected (see Figure 12).

- Cation-exchange fractions that cross-reacted with the antiserum (fractions 14-28, Figure 12)
30 were then further purified by reverse phase chromatography. Cross-reacting fractions were loaded onto a 7 µm C18 reverse phase column (Brownlee) equilibrated with 90% H₂O, 10% acetonitrile and 0.1% Trifluoroacetic acid (TFA)(=100%A). Bound proteins were eluted with a linear gradient from 100%A to 100%B (5% H₂O, 95% acetonitrile, 0.08% TFA). The absorbance of the eluted proteins was monitored at 214nm and 280nm. The eluted proteins were dried under vacuum and resuspended

in water three times to remove traces of TFA from the samples. Reverse phase protein elution fractions 20 to 61 were analysed by pooling 2 adjacent fractions and performing a western blot analysis (see Figure 13). Fractions 22-41 gave a weak positive reaction and fractions 42-57 gave a strong positive reaction to the anti-MiAMP2c antiserum. Fractions that showed antifungal activity against *S.sclerotiorum* at 50 µg/ml and 10 µg/ml are indicated by arrows on the chromatogram.

Using the approach above, several active fractions (termed SsAMP1 and SsAMP2) were obtained which were assessed for their antifungal activity against *Sclerotinia sclerotiorum*, *Alternaria brassicola*, *Leptosphaeria maculans*, *Verticilium dahliae* and *Fusarium oxysporum*. Bioassays were carried out as described in Example 2 and results shown in Example 15. Another fragment which reacted with MiAMP2 antiserum was purified and sequenced (SsAMP3) but insufficient protein was available for characterisation of antimicrobial activity. Partial sequences obtained from these proteins are shown in Figure 4 (SEQ ID NOS: 26, 27 and 28). Full sequencing of the peptides or cloning of cDNAs encoding the seed storage proteins from this species will reveal the extent of homology between these peptides and MiAMP2-series homologues.

Example 14

Synthesis of small fragments of MiAMP2c

In an effort to determine if the full MiAMP2c molecule was absolutely necessary for the protein to exhibit antimicrobial activity, two separate peptides were chemically synthesized by Auspep Pty. Ltd. (Australia). For each peptide, the cysteine residues were changed to alanine residues so that disulfide bonds were no longer capable of being formed between two separate protein chains. Tyrosine residues were also changed to alanine since it was expected that tyrosine also participated in the helix-turn-helix stabilization and this would not be needed in the synthetic peptides lacking one of the helices. Alanine is also favorable to the formation of alpha-helices so it should not interfere with the native helical structure to a large degree. Peptide one is comprised of 22 amino acids from 118 to 139 in the amino acid sequence of clone 3 (sequence: RQRDP QQQAE QAQKR AQRRE TE, SEQUENCE ID NO: 9). Peptide 2 is 25 amino acids in length and runs from 140 to 164 in clone 3 (sequence: PRHMQ IAQQR AERRA EKEKR KQQKR, SEQ ID NO: 10). Peptides 1 and 2 are labeled MiAMP2c pep1 and MiAMP2c pep2 respectively. These peptides were resuspended in Milli-Q water and bioassayed against a number of fungi. As seen in Table 2, peptide 2 has inhibitory activity against a variety of fungi whereas peptide 1 exhibited little or no activity. Mixtures of peptide 1 and peptide 2 exhibit similar levels of activity as seen with peptide 2 alone indicating that only peptide 2 is exhibiting activity. The fact that peptide 2 exhibits antimicrobial activity in the absence of the helix-turn-helix structure exhibited by MiAMP2c reveals that the helix-turn-helix structure is not absolutely necessary for the peptides to retain activity. Nevertheless,

peptide 2 did not exhibit the same degree of activity on a molar basis as MiAMP2c (whole fragment) indicating that the helix-turn-helix structure is important for maximal expression of antimicrobial activity by the fragments involved. It is also expected that the helix-turn-helix structure will confer greater stability to the MiAMP2 homologues, thus rendering these proteins less susceptible to proteolytic cleavage and other forms of degradation. Greater stability would lead to maintaining antimicrobial activity over a longer period of time.

Example 15

Antifungal activity of MiAMP2c homologues and fragment(s)

MiAMP2c and each of the various MiAMP2 homologues were tested against a variety of fungi as concentrations ranging from 2 to 50 µg/ml. Table 1 shows the IC₅₀ value of pure MiAMP2c against various fungi and bacteria. In the table, the ">50" indicates that 50% inhibition of the fungus was not achieved at 50 µg/ml which was the highest concentration tested. The abbreviation "ND" indicates that the test was not performed or that results could not be interpreted. The antimicrobial activity of MiAMP2c was also tested in the presence of 1 mM Ca²⁺ in the test medium and the IC₅₀ values for these tests are given in the right-hand column. As can be seen in the table, the inhibitory activity of MiAMP2c is greatly reduced (although not eliminated) in the presence of Ca²⁺.

Table 1

Concentrations of MiAMP2c at which 50% inhibition of growth was observed

Organism	IC ₅₀ (µg/ml)	IC ₅₀ + Ca ²⁺ (µg/ml)
<i>Alternaria helianthi</i>	5-10	ND
<i>Candida albicans</i>	>50	>50
<i>Ceratocystis paradoxa</i>	20-50	>50
<i>Cercospora nicotianae</i>	5-10	5-10
<i>Clavibacter michiganensis</i>	50	>50
<i>Chalara elegans</i>	2-5	10-20
<i>Fusarium oxysporum</i>	10	20-50
<i>Sclerotinia sclerotiorum</i>	20-50	>50
<i>Phytophthora cryptogea</i>	5-10	10-25
<i>Phytophthora parasitica nicotiana</i>	10-20	>50

	30	
<i>Verticillium dahliae</i>	5-10	>50
<i>Ralstonia solanacearum</i>	>50	>50
<i>Pseudomonas syringae tabaci</i>	>50	>50
<i>Saccharomyces cerevisiae</i>	20-50	>50
<i>Escherichia coli</i>	>50	>50

Table 2 shows the the antimicrobial activity of various homologues and fragments of MiAMP2c. In the table, the following abbreviations are used: Ab, *Alternaria brassicola*; Cp: *Ceratocystis paradoxa*; Foc: *Fusarium oxysporum*; Lm: *Leptosphaeria maculans*; Ss: *Sclerotinia sclerotiorum*; Vd: *Verticillium dahliae*. The ">50" indicates that concentrations higher than 50 µg/ml were not tested so that an IC₅₀ value could not be established. A blank space indicates that the test was not performed or that results could not be interpreted.

The TcAMP1 and 2 used for the results presented in Table 2 were derived from cocoa vicilin (Examples 10 and 11). SsAMP1 and 2 show reactivity with MiAMP2c antibodies and also exhibit antimicrobial activity as seen in the table below. The versions of MiAMP2a, b and d as well as TcAMP1 and TcAMP2 tested in the bioassays all contain a His tag fusion resulting from expression in the vector pET16b. MiAMP2c pep1 and 2 are the N and C terminal regions, respectively, of MiAMP2c antimicrobial peptide as specified in Example 14 above. The concentration value listed for 'MiAMP2c pep1+2' is the concentration of each individual peptide in the mixture. It should be remembered that MiAMP2c pep1 and pep2 are both about ½ the size of MiAMP2c; comparisons of the activity of these peptides with the MiAMP2c protein should, therefore, be made on a molar basis rather than on a strict µg/ml concentration basis. Peptides were only tested in media A which did not contain added Ca²⁺.

Table 2

IC₅₀ values (µg/ml) of MiAMP2 related proteins against various fungi

Peptide tested	Fungus used in bioassay					
	Ab	Cp	Foc	Lm	Ss	Vd
MiAMP2a			5-10	2.5-5	5-10	
MiAMP2b			2.5	2.5	5-10	
MiAMP2c		20-50	10		20-50	5-10
MiAMP2d			5	2.5	5-10	
MiAMP2c pep1			100		>50	

		31			
MiAMP2c pep2		10-20	10-20	50	10-20
MiAMP2c pep1+2		10-25		50	
TcAMP1	10	5-10	2-5	10	5-20
TcAMP2	5-10	5-10	2-5	5	5-20
SsAMP1		20-50	20-50	20-50	10-20
SsAMP2	20-50	>50	>50	>50	>50

It is worthy of note that while the TcAMP1 and 2 sequences are readily available in the public data bases, no antimicrobial activity had ever been assigned to them. These sequences were derived from much larger proteins involved in seed storage functions. The inventors have thus described a completely new activity for a small portion of the overall cocoa vicilin molecules. The activity of cotton fragments 1, 2, and 3 has been exemplified by other authors (Chung, R. P.T. *et al.* [1997] *Plant Science* 127:1-16).

Example 16

Construction of the plant transformation vector PCV91-MiAMP2c

The expression vector pPCV91-MiAMP2c (Figure 14) contains the full coding region of the MiAMP2c (Example 7) DNA flanked at its 5' end by the strong constitutive promoter of 35S RNA from the cauliflower mosaic virus (pCaMV35S) (Odel *et al.*, [1985] *Nature* 313: 810-812) with a quadruple-repeat enhancer element (e-35S) to allow for high transcriptional activity (Kay *et al.* [1987] *Science* 236:1299-1302). The coding region of MiAMP2c DNA is flanked at its 3' end by the polyadenylation sequence of 35S RNA of the cauliflower mosaic virus (pA35S). The plasmid backbone of this vector is the plasmid pPCV91 (Walden, R. *et al.* [1990] *Methods Mol. Cell. Biol.* 1:175-194). The plasmid also contains other elements useful for plant transformation such as an ampicillin resistance gene (bla) and a hygromycin resistance gene (hph) driven by the nos promoter (pnos). These and other features allow for selection in various cloning and transformation procedures. The plasmid pPCV91-MiAMP2c was constructed as follows: A cloned fragment encoding MiAMP2c (Example 7) was digested using restriction enzymes to release the MiAMP2c gene fragment containing a synthetic leader sequence.. The binary vector pPCV91 was digested with the restriction enzyme *Bam* HI. Both the MiAMP2c DNA fragment containing and the binary vector were ligated using T4 DNA ligase to produce pPCV91-MiAMP2c binary vector for plant transformation (Figure 12).

Using this approach, other homologues of MiAMP2c can be expressed in plants. Not only can individual homologues be expressed, but they may be expressed in combination with other proteins as fusion proteins or as portions of larger precursor proteins. For example, it is possible to express

the N-terminal region of MiAMP2 clone 1 (amino acids 1 to ~246) which contains a signal peptide and the hydrophilic region containing four antimicrobial segments. Transgenic plants can then be assessed to examine whether the individual fragments are being processed into the expected fragments by the processing machinery already present in the plant cells. It is also possible to
5 express the entire MiAMP2 clone 1 (amino acids 1 to 666) and to examine the processing of the entire protein when expressed in transgenic plants. Homologous regions from other sequences can also be used in multiple combinations with, for example, ten (10) or more MiAMP2-like fragments expressed as one large fusion protein with acidic cleavage sites located at proper locations between each of the fragments. As well as linking MiAMP2 fragments together, it would also be possible to
10 link MiAMP2 fragments to other useful proteins for expression in plants.

Example 17

Transgenic plants expressing MiAMP2c (or related fragments)

The disarmed *Agrobacterium tumefaciens* strain GV3101 (pMP90RK) (Koncz, Cs.[1986] *Mol. Gen. Genet.* 204:383-396) was transformed with the vector pPCV91-MiAMP2c (Example 16) using
15 the method of Walkerpeach *et al.* (Plant Mol. Biol. Manual B1:1-19 [1994]) adapted from Van Haute *et al* (*EMBO J.* 2:411-417 1983)].

Tobacco transformation was carried out using leaf discs of *Nicotiana tabacum* based on the method of Horsch *et al.* (*Science* 227:1229-1231 [1985]) and co-culturing strains containing pPCV91-MiAMP2c. After co-cultivation of *Agrobacterium* and tobacco leaf disks, transgenic plants
20 (transformed with pPCV91-MiAMP2c) were regenerated on media containing 50 µg/ml hygromycin and 500 µg/ml Cefotaxime. These transgenic plants were analysed for expression of the newly-introduced genes using standard western blotting techniques (Figure 15). Figure 15 shows a western blot of extracts from transgenic tobacco carrying the construct for MiAMP2c from example 16. Lane 1 contains pure MiAMP2c as a standard, lanes 2 and 3 contain extracts from transgenic plants
25 carrying the pPCV91-MiAMP2c construct. As can be seen in the figure, faint bands are present at approximately the correct molecular weight, indicating that the transgenic plants appear to be expressing the MiAMP2c protein. Plants capable of constitutive expression of the introduced genes may be selected and self-pollinated to give seed. F1 seedlings of the transgenic plants may be
30 further analysed.

Example 18

MiAMP2c Homologues

Every homologue of MiAMP2c that has been tested has exhibited some antimicrobial activity. This evidence indicates that other homologues will also exhibit antimicrobial activity. These homologues include fragments from 1) peanut (Burks, A.W. *et al.* [1995] *J. Clin. Invest.* 96 (4),

1715-1721), 2) maize (Belanger, F.C. and Kriz, A.L.[1991] *Genetics* 129 (3), 863-872), 3) barley (Heck, G.R. *et al.* [1993] *Mol. Gen. Genet.* 239 (1-2), 209-218), and 4) soybean (Sebastiani, F.L. *et al.* [1990] *Plant Mol. Biol.* 15 (1), 197-201). (see SEQ ID NOS: 21, 22, 24, and 25). Other sequences derived from seed storage proteins of the 7S class are also expected to yield homologues
5 of MiAMP2 proteins.

SEQUENCE LISTINGS

5 (1) GENERAL INFORMATION:

(i) APPLICANT:

(A) NAME: COOPERATIVE RESEARCH CENTRE FOR TROPICAL PLANT
PATHOLOGY

10 (B) STREET: The University of Queensland

(C) CITY: St Lucia

(D) STATE: Queensland

(E) COUNTRY: Australia

(F) POSTAL CODE (ZIP): 4067

15

(ii) TITLE OF INVENTION: Antimicrobial Protein

(iii) NUMBER OF SEQUENCES: 28

(iv) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk

(B) COMPUTER: IBM PC compatible

(C) OPERATING SYSTEM: PC-DOS/MS-DOS

25

(D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 666 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Macadamia integrifolia*

(F) TISSUE TYPE: Seeds

40

(xi) SEQUENCE DESCRIPTION: SEO ID NO: 1:

Met Ala Ile Asn Thr Ser Asn Leu Cys Ser Leu Leu Phe Leu Leu Ser
1 5 10 15

45

Leu Phe Leu Leu Ser Thr Thr Val Ser Leu Ala Glu Ser Glu Phe Asp
20 25 30

Arg Gln Glu Tyr Glu Glu Cys Lys Arg Gln Cys Met Gln Leu Glu Thr
35 40 45

50

Ser Gly Gln Met Arg Arg Cys Val Ser Gln Cys Asp Lys Arg Phe Glu
50 55 60

55 Glu Asp Ile Asp Trp Ser Lys Tyr Asp Asn Gln Glu Asp Pro Gln Thr

35

	65		70		75		80
	Glu Cys Gln Gln Cys Gln Arg Arg Cys Arg Gln Gln Glu Ser Gly Pro						
		85		90		95	
5	Arg Gln Gln Gln Tyr Cys Gln Arg Arg Cys Lys Glu Ile Cys Glu Glu						
		100		105		110	
10	Glu Glu Glu Tyr Asn Arg Gln Arg Asp Pro Gln Gln Gln Tyr Glu Gln						
		115		120		125	
	Cys Gln Lys His Cys Gln Arg Arg Glu Thr Glu Pro Arg His Met Gln						
		130		135		140	
15	Thr Cys Gln Gln Arg Cys Glu Arg Arg Tyr Glu Lys Glu Lys Arg Lys						
		145		150		155	160
	Gln Gln Lys Arg Tyr Glu Glu Gln Gln Arg Glu Asp Glu Glu Lys Tyr						
20		165		170		175	
	Glu Glu Arg Met Lys Glu Glu Asp Asn Lys Arg Asp Pro Gln Gln Arg						
		180		185		190	
25	Glu Tyr Glu Asp Cys Arg Arg Arg Cys Glu Gln Gln Glu Pro Arg Gln						
		195		200		205	
	Gln His Gln Cys Gln Leu Arg Cys Arg Glu Gln Gln Arg Gln His Gly						
		210		215		220	
30	Arg Gly Gly Asp Met Met Asn Pro Gln Arg Gly Gly Ser Gly Arg Tyr						
		225		230		235	240
	Glu Glu Gly Glu Glu Glu Gln Ser Asp Asn Pro Tyr Tyr Phe Asp Glu						
35		245		250		255	
	Arg Ser Leu Ser Thr Arg Phe Arg Thr Glu Glu Gly His Ile Ser Val						
		260		265		270	
40	Leu Glu Asn Phe Tyr Gly Arg Ser Lys Leu Leu Arg Ala Leu Lys Asn						
		275		280		285	
	Tyr Arg Leu Val Leu Leu Glu Ala Asn Pro Asn Ala Phe Val Leu Pro						
		290		295		300	
45	Thr His Leu Asp Ala Asp Ala Ile Leu Leu Val Ile Gly Gly Arg Gly						
		305		310		315	320
	Ala Leu Lys Met Ile His His Asp Asn Arg Glu Ser Tyr Asn Leu Glu						
50		325		330		335	
	Cys Gly Asp Val Ile Arg Ile Pro Ala Gly Thr Thr Phe Tyr Leu Ile						
		340		345		350	
55	Asn Arg Asp Asn Asn Glu Arg Leu His Ile Ala Lys Phe Leu Gln Thr						
		355		360		365	

36

	Ile	Ser	Thr	Pro	Gly	Gln	Tyr	Lys	Glu	Phe	Phe	Pro	Ala	Gly	Gly	Gln
	370							375				380				
5	Asn	Pro	Glu	Pro	Tyr	Leu	Ser	Thr	Phe	Ser	Lys	Glu	Ile	Leu	Glu	Ala
	385					390					395					400
	Ala	Leu	Asn	Thr	Gln	Thr	Glu	Lys	Leu	Arg	Gly	Val	Phe	Gly	Gln	Gln
					405					410					415	
10	Arg	Glu	Gly	Val	Ile	Ile	Arg	Ala	Ser	Gln	Glu	Gln	Ile	Arg	Glu	Leu
				420					425					430		
	Thr	Arg	Asp	Asp	Ser	Glu	Ser	Arg	His	Trp	His	Ile	Arg	Arg	Gly	Gly
15			435					440					445			
	Glu	Ser	Ser	Arg	Gly	Pro	Tyr	Asn	Leu	Phe	Asn	Lys	Arg	Pro	Leu	Tyr
		450					455					460				
20	Ser	Asn	Lys	Tyr	Gly	Gln	Ala	Tyr	Glu	Val	Lys	Pro	Glu	Asp	Tyr	Arg
	465					470					475					480
	Gln	Leu	Gln	Asp	Met	Asp	Leu	Ser	Val	Phe	Ile	Ala	Asn	Val	Thr	Gln
				485						490					495	
25	Gly	Ser	Met	Met	Gly	Pro	Phe	Phe	Asn	Thr	Arg	Ser	Thr	Lys	Val	Val
				500					505					510		
	Val	Val	Ala	Ser	Gly	Glu	Ala	Asp	Val	Glu	Met	Ala	Cys	Pro	His	Leu
30			515					520					525			
	Ser	Gly	Arg	His	Gly	Gly	Arg	Gly	Gly	Gly	Lys	Arg	His	Glu	Glu	Glu
		530					535					540				
35	Glu	Asp	Val	His	Tyr	Glu	Gln	Val	Arg	Ala	Arg	Leu	Ser	Lys	Arg	Glu
	545					550					555					560
	Ala	Ile	Val	Val	Leu	Ala	Gly	His	Pro	Val	Val	Phe	Val	Ser	Ser	Gly
					565					570					575	
40	Asn	Glu	Asn	Leu	Leu	Leu	Phe	Ala	Phe	Gly	Ile	Asn	Ala	Gln	Asn	Asn
				580					585					590		
	His	Glu	Asn	Phe	Leu	Ala	Gly	Arg	Glu	Arg	Asn	Val	Leu	Gln	Gln	Ile
45			595					600					605			
	Glu	Pro	Gln	Ala	Met	Glu	Leu	Ala	Phe	Ala	Ala	Pro	Arg	Lys	Glu	Val
		610					615					620				
50	Glu	Glu	Ser	Phe	Asn	Ser	Gln	Asp	Gln	Ser	Ile	Phe	Phe	Pro	Gly	Pro
	625					630					635					640
	Arg	Gln	His	Gln	Gln	Gln	Ser	Pro	Arg	Ser	Thr	Lys	Gln	Gln	Gln	Pro
					645					650					655	
55	Leu	Val	Ser	Ile	Leu	Asp	Phe	Val	Gly	Phe						
				660					665							

(2) INFORMATION FOR SEQ ID NO: 2:

5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2171 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Macadamia integrifolia*
15 (F) TISSUE TYPE: Seeds

(ix) FEATURE:
 (A) NAME/KEY: sig_peptide
20 (B) LOCATION:1..85

(x) FEATURE:
 (A) NAME/KEY: mat_peptide
 (B) LOCATION:86..1999

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

ATGGCGATCA ATACATCAA TTTATGTTCT CTTCTCTTTC TCCTTTCACT CTTCTTCTG	60
30 TCTACGACAG TGTCTCTTGC TGAAAGTGAA TTTGACAGGC AGGAATATGA GGAGTGCAAA	120
CGGCAATGCA TGCAGTTGGA GACATCAGGC CAGATGCGTC GGTGTGTGAG TCAGTGCGAT	180
AAGAGATTTG AAGAGGATAT AGATTGGTCT AAGTATGATA ACCAAGAGGA TCCTCAGACG	240
35 GAATGCCAAC AATGCCAGAG GCGATGCAGG CAGCAGGAGA GTGGCCCACG TCAGCAACAA	300
TACTGCCAAC GACGCTGCAA GGAAATATGT GAAGAAGAAG AAGAATATAA CCGACAACGT	360
40 GATCCACAGC AGCAATACGA GCAATGTCAG AAGCACTGCC AACGGCGCGA GACAGAGCCA	420
CGTCACATGC AAACATGTCA ACAACGCTGC GAGAGGAGAT ATGAAAAGGA GAAACGTAAG	480
CAACAAAAGA GATATGAAGA GCAACAACGT GAAGACGAAG AGAAATATGA AGAGCGAATG	540
45 AAGGAAGAAG ATAACAAACG CGATCCACAA CAAAGAGAGT ACGAAGACTG CCGGAGGCGC	600
TGCGAACAAAC AGGAGCCACG TCAGCAGCAC CAGTGCCAGC TAAGATGCCG AGAGCAGCAG	660
50 AGGCAACACG GCCGAGGTGG CGATATGATG AACCCTCAGA GGGGAGGCAG CGGCAGATAC	720
GAGGAGGGAG AAGAGGAGCA AAGCGACAAC CCCTACTACT TCGACGAACG AAGCTTAAGT	780
ACAAGGTTCA GGACCGAGGA AGGCCACATC TCAGTTCTGG AGAACTTCTA TGGTAGATCC	840
55 AAGCTTCTAC GCGCACTAAA AACTATCGC TTGGTGCTCC TCGAGGCTAA CCCCACGCC	900

	TTCGTGCTCC CTACCCACTT GGATGCAGAT GCCATTCTCT TGGTCATAGG AGGGAGAGGA	960
5	GCCCTCAAAA TGATCCACCA CGACAACAGA GAATCCTACA ACCTCGAGTG TGGAGACGTA	1020
	ATCAGAATCC CAGCTGGAAC CACATTCTAC TTAATCAACC GAGACAACAA CGAGAGGCTC	1080
	CACATAGCCA AGTTCTTACA GACCATATCC ACTCCTGGCC AATACAAGGA ATTCTTCCCA	1140
10	GCTGGAGGCC AAAACCCAGA GCCGTACCTC AGTACCTTCA GCAAAGAGAT TCTCGAGGCT	1200
	GCGCTCAACA CACAAACAGA GAAGCTGCGT GGGGTGTTTG GACAGCAAAG GGAGGGAGTG	1260
15	ATAATTAGGG CGTCACAGGA GCAGATCAGG GAGTTGACTC GAGATGACTC AGAGTCACGA	1320
	CACTGGCATA TAAGGAGAGG TGGTGAATCA AGCAGGGGAC CTTACAATCT GTTCAACAAA	1380
	AGGCCACTGT ACTCCAACAA ATACGGTCAA GCCTACGAAG TCAAACCTGA GGA CTACAGG	1440
20	CAACTCCAAG ACATGGACTT ATCGGTTTTT ATAGCCAACG TCACCCAGGG ATCCATGATG	1500
	GGTCCCTTCT TCAACACTAG GTCTACAAAG GTGGTAGTGG TGGCTAGTGG AGAGGCAGAT	1560
25	GTGGAAATGG CATGCCCTCA CTTGTCGGGA AGACACGGCG GCCGCGGTGG AGGAAAAAGG	1620
	CATGAGGAGG AAGAGGATGT GCACTATGAG CAGGTTAGAG CACGTTTGTC GAAGAGAGAG	1680
	GCCATTGTTG TTCTGGCAGG TCATCCCGTC GTCTTCGTTT CATCCGAAA CGAGAACCTG	1740
30	CTGCTTTTTG CATTGGAAT CAATGCCCAA AACACCACG AGAACTTCCT CGCGGGGAGA	1800
	GAGAGGAACG TGCTGCAGCA GATAGAGCCA CAGGCAATGG AGCTAGCGTT TGCCGCTCCA	1860
35	AGGAAAGAGG TAGAAGAGTC ATTTAACAGC CAGGACCAGT CTATCTTCTT TCCTGGGCCC	1920
	AGGCAGCACC AGCAACAGTC GCCCCGCTCC ACCAAGCAAC AACAGCCTCT CGTCTCCATT	1980
	CTGGACTTCG TTGGCTTCTA AAGTTCCACA AAAAAGAGTG TGTTATGTAG TATAGGTTAG	2040
40	TAGCTCCTAG CTCGGTGTAT GAGAGTGGTA AGAGACTAAG ACGCTAAATC CCTAAGTAAC	2100
	TAACCTGGCG AGCTTGCGTG TATGCAAATA AAGAGGAACA GCTTTCCAAC TTTAAAAAAA	2160
45	AAAAAAAAA A	2171

(2) INFORMATION FOR SEQ ID NO: 3:

- (i) SEQUENCE CHARACTERISTICS:
- 50 (A) LENGTH: 666 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- 55 (ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Macadamia integrifolia*
 (F) TISSUE TYPE: Seeds

5

(ix) FEATURE:
 (A) NAME/KEY: sig_peptide
 (B) LOCATION:1..28

10

(ix) FEATURE:
 (A) NAME/KEY: mat_peptide
 (B) LOCATION:29..666

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

Met	Ala	Ile	Asn	Thr	Ser	Asn	Leu	Cys	Ser	Leu	Leu	Phe	Leu	Leu	Ser	1	5	10	15
Leu	Phe	Leu	Leu	Ser	Thr	Thr	Val	Ser	Leu	Ala	Glu	Ser	Glu	Phe	Asp	20	25	30	
Arg	Gln	Glu	Tyr	Glu	Glu	Cys	Lys	Arg	Gln	Cys	Met	Gln	Leu	Glu	Thr	35	40	45	
Ser	Gly	Gln	Met	Arg	Arg	Cys	Val	Ser	Gln	Cys	Asp	Lys	Arg	Phe	Glu	50	55	60	
Glu	Asp	Ile	Asp	Trp	Ser	Lys	Tyr	Asp	Asn	Gln	Asp	Asp	Pro	Gln	Thr	65	70	75	80
Asp	Cys	Gln	Gln	Cys	Gln	Arg	Arg	Cys	Arg	Gln	Gln	Glu	Ser	Gly	Pro	85	90	95	
Arg	Gln	Gln	Gln	Tyr	Cys	Gln	Arg	Arg	Cys	Lys	Glu	Ile	Cys	Glu	Glu	100	105	110	
Glu	Glu	Glu	Tyr	Asn	Arg	Gln	Arg	Asp	Pro	Gln	Gln	Gln	Tyr	Glu	Gln	115	120	125	
Cys	Gln	Glu	Arg	Cys	Gln	Arg	His	Glu	Thr	Glu	Pro	Arg	His	Met	Gln	130	135	140	
Thr	Cys	Gln	Gln	Arg	Cys	Glu	Arg	Arg	Tyr	Glu	Lys	Glu	Lys	Arg	Lys	145	150	155	160
Gln	Gln	Lys	Arg	Tyr	Glu	Glu	Gln	Gln	Arg	Glu	Asp	Glu	Glu	Lys	Tyr	165	170	175	
Glu	Glu	Arg	Met	Lys	Glu	Glu	Asp	Asn	Lys	Arg	Asp	Pro	Gln	Gln	Arg	180	185	190	
Glu	Tyr	Glu	Asp	Cys	Arg	Arg	Arg	Cys	Glu	Gln	Gln	Glu	Pro	Arg	Gln	195	200	205	
Gln	Tyr	Gln	Cys	Gln	Arg	Arg	Cys	Arg	Glu	Gln	Gln	Arg	Gln	His	Gly	210	215	220	

	Arg Gly Gly Asp Leu Ile Asn Pro Gln Arg Gly Gly Ser Gly Arg Tyr	
	225	230 235 240
5	Glu Glu Gly Glu Glu Lys Gln Ser Asp Asn Pro Tyr Tyr Phe Asp Glu	
		245 250 255
	Arg Ser Leu Ser Thr Arg Phe Arg Thr Glu Glu Gly His Ile Ser Val	
		260 265 270
10	Leu Glu Asn Phe Tyr Gly Arg Ser Lys Leu Leu Arg Ala Leu Lys Asn	
		275 280 285
	Tyr Arg Leu Val Leu Leu Glu Ala Asn Pro Asn Ala Phe Val Leu Pro	
15		290 295 300
	Thr His Leu Asp Ala Asp Ala Ile Leu Leu Val Thr Gly Gly Arg Gly	
		305 310 315 320
20	Ala Leu Lys Met Ile His Arg Asp Asn Arg Glu Ser Tyr Asn Leu Glu	
		325 330 335
	Cys Gly Asp Val Ile Arg Ile Pro Ala Gly Thr Thr Phe Tyr Leu Ile	
		340 345 350
25	Asn Arg Asp Asn Asn Glu Arg Leu His Ile Ala Lys Phe Leu Gln Thr	
		355 360 365
	Ile Ser Thr Pro Gly Gln Tyr Lys Glu Phe Phe Pro Ala Gly Gly Gln	
30		370 375 380
	Asn Pro Glu Pro Tyr Leu Ser Thr Phe Ser Lys Glu Ile Leu Glu Ala	
		385 390 395 400
35	Ala Leu Asn Thr Gln Ala Glu Arg Leu Arg Gly Val Leu Gly Gln Gln	
		405 410 415
	Arg Glu Gly Val Ile Ile Ser Ala Ser Gln Glu Gln Ile Arg Glu Leu	
		420 425 430
40	Thr Arg Asp Asp Ser Glu Ser Arg Arg Trp His Ile Arg Arg Gly Gly	
		435 440 445
	Glu Ser Ser Arg Gly Pro Tyr Asn Leu Phe Asn Lys Arg Pro Leu Tyr	
45		450 455 460
	Ser Asn Lys Tyr Gly Gln Ala Tyr Glu Val Lys Pro Glu Asp Tyr Arg	
		465 470 475 480
50	Gln Leu Gln Asp Met Asp Val Ser Val Phe Ile Ala Asn Ile Thr Gln	
		485 490 495
	Gly Ser Met Met Gly Pro Phe Phe Asn Thr Arg Ser Thr Lys Val Val	
		500 505 510
55	Val Val Ala Ser Gly Glu Ala Asp Val Glu Met Ala Cys Pro His Leu	

41

515 520 525

Ser Gly Arg His Gly Gly Arg Arg Gly Gly Lys Arg His Glu Glu Glu
530 535 540

Glu Asp Val His Tyr Glu Gln Val Lys Ala Arg Leu Ser Lys Arg Glu
545 550 555 560

Ala Ile Val Val Pro Val Gly His Pro Val Val Phe Val Ser Ser Gly
565 570 575

Asn Glu Asn Leu Leu Leu Phe Ala Phe Gly Ile Asn Ala Gln Asn Asn
580 585 590

His Glu Asn Phe Leu Ala Gly Arg Glu Arg Asn Val Leu Gln Gln Ile
595 600 605

Glu Pro Gln Ala Met Glu Leu Ala Phe Ala Ala Pro Arg Lys Glu Val
610 615 620

Glu Glu Leu Phe Asn Ser Gln Asp Glu Ser Ile Phe Phe Pro Gly Pro
625 630 635 640

Arg Gln His Gln Gln Gln Ser Ser Arg Ser Thr Lys Gln Gln Gln Pro
645 650 655

Leu Val Ser Ile Leu Asp Phe Val Gly Phe
660 665

30

(2) INFORMATION FOR SEQ ID NO: 4:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2171 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Macadamia integrifolia*
- (F) TISSUE TYPE: Seeds
- (ix) FEATURE:
- (A) NAME/KEY: sig_peptide
- (B) LOCATION:1..86
- (ix) FEATURE:
- (A) NAME/KEY: mat_peptide
- (B) LOCATION:87..1999
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

55

ATGGCGATCA ATACATCAAA TTTATGTTCT CTTCTCTTTC TCCTTCCCT CTCCTTCTG

60

	TCAACGACAG	TGTCTCTTGC	TGAAAGTGAA	TTTGACAGGC	AGGAATATGA	GGAGTGCAAA	120
5	CGGCAATGCA	TGCAGTTGGA	GACATCAGGC	CAGATGCGTC	GGTGTGTGAG	TCAGTGCGAT	180
	AAGAGATTTG	AAGAGGATAT	AGATTGGTCT	AAGTATGATA	ACCAAGACGA	TCCTCAGACG	240
	GATTGCCAAC	AATGCCAGAG	GCGATGCAGG	CAGCAGGAGA	GTGGCCCACG	TCAGCAACAA	300
10	TACTGCCAAC	GACGCTGCAA	GGAAATATGT	GAAGAAGAAG	AAGAATATAA	CCGACAACGT	360
	GATCCACAGC	AGCAATACGA	GCAATGTCAG	GAGCGCTGCC	AACGGCACGA	GACAGAGCCA	420
15	CGTCACATGC	AAACATGTCA	ACAACGCTGC	GAGAGGAGAT	ATGAAAAGGA	GAAACGTAAG	480
	CAACAAAAGA	GATATGAAGA	GCAACAACGT	GAAGACGAAG	AGAAATATGA	AGAGCGAATG	540
	AAGGAAGAAG	ATAACAAACG	CGATCCACAA	CAAAGAGAGT	ACGAAGACTG	CCGGAGGCGC	600
20	TGCGAACAAAC	AGGAGCCACG	TCAGCAGTAC	CAGTGCCAGC	GAAGATGCCG	AGAGCAGCAG	660
	AGGCAACACG	GCCGAGGTGG	TGATTTGATT	AACCCTCAGA	GGGAGGCAG	CGGCAGATAC	720
25	GAGGAGGGAG	AAGAGAAGCA	AAGCGACAAC	CCCTACTACT	TCGACGAACG	AAGCTTAAGT	780
	ACAAGGTTCA	GGACCGAGGA	AGGCCACATC	TCAGTTCTGG	AGAACTTCTA	TGGTAGATCC	840
	AAGCTTCTAC	GCGCACTAAA	AACTATCGC	TTGGTGCTCC	TCGAGGCTAA	CCCCAACGCC	900
30	TTCGTGCTCC	CTACCCACTT	GGACGCAGAT	GCCATTCTCT	TGGTCACCGG	AGGGAGAGGA	960
	GCCCTCAAAA	TGATCCACCG	TGACAACAGA	GAATCCTACA	ACCTCGAGTG	TGGAGACGTA	1020
35	ATCAGAATCC	CAGCTGGAAC	CACATTCTAC	TTAATCAACC	GAGACAACAA	CGAGAGGCTC	1080
	CACATAGCCA	AGTTCTTACA	GACCATATCC	ACTCCTGGCC	AATACAAGGA	ATTCTTCCCA	1140
	GCTGGAGGCC	AAAACCCAGA	GCCGTACCTC	AGTACCTTCA	GCAAAGAGAT	TCTCGAGGCT	1200
40	GCGCTCAACA	CACAAGCAGA	GAGGCTGCGT	GGGGTGCTTG	GACAGCAAAG	GGAGGGAGTG	1260
	ATAATTAGTG	CGTCACAGGA	GCAGATCAGG	GAGTTGACTC	GAGATGACTC	AGAGTCACGA	1320
45	CGCTGGCATA	TAAGGAGAGG	TGGTGAATCA	AGCAGGGGAC	CTTACAATCT	GTTCAACAAA	1380
	AGGCCACTGT	ACTCCAACAA	ATACGGTCAA	GCCTACGAAG	TCAAACCTGA	GGACTACAGG	1440
	CAACTCCAAG	ACATGGACGT	ATCGGTTTTC	ATAGCCAACA	TCACCCAGGG	ATCCATGATG	1500
50	GGTCCCTTCT	TCAACACTAG	GTCTACAAAG	GTGGTAGTGG	TGGCTAGTGG	AGAGGCAGAT	1560
	GTGGAAATGG	CATGCCCTCA	CTTGTCGGGA	AGACACGGCG	GCCGCCGTGG	AGGGAAAAGG	1620
55	CATGAGGAGG	AAGAGGATGT	GCACTATGAG	CAGGTTAAAG	CACGTTTGTC	GAAGAGAGAG	1680
	GCCATTGTTG	TTCCGGTAGG	TCATCCCGTC	GTCTTCGTTT	CATCCGGAAA	CGAGAACCCTG	1740

CTGCTTTTGT CATTGGAAT CAATGCCCAA AACAAACCAG AGAACTTCCT CGCGGGGAGA 1800
 GAGAGGAACG TGCTGCAGCA GATAGAGCCA CAGGCAATGG AGCTAGCGTT TGCCGCTCCA 1860
 5 AGGAAAGAGG TAGAAGAGTT ATTTAACAGC CAGGACGAGT CTATCTTCTT TCCTGGGCCC 1920
 AGGCAGCACC AGCAACAGTC TTCCCGCTCC ACCAAGCAAC AACAGCCTCT CGTCTCCATT 1980
 10 CTGGACTTCG TTGGCTTCTA AAGTTCTACA AAAAAGAGTG TGTATGTAG TATAGGTTAG 2040
 TAGCTCCTAG CTCGGTGTAT GCGAGTGGTA AGAGACCAAG ACGCTAAATC CCTAAGTAAC 2100
 TAACCTGGCG AGCTTGC GTG TATGCAAATA AAGAGGAACA GCTTTCCAAC TTTAAAAAAA 2160
 15 AAAAAAAAAA A 2171

(2) INFORMATION FOR SEQ ID NO: 5:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 625 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

25

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

30

(A) ORGANISM: *Macadamia integrifolia*

(F) TISSUE TYPE: Seeds

(ix) FEATURE:

35

(A) NAME/KEY: partial mat_peptide

(B) LOCATION:1..625

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

40

Gln Cys Met Gln Leu Glu Thr Ser Gly Gln Met Arg Arg Cys Val Ser
 1 5 10 15

Gln Cys Asp Lys Arg Phe Glu Glu Asp Ile Asp Trp Ser Lys Tyr Asp
 20 25 30

45

Asn Gln Glu Asp Pro Gln Thr Glu Cys Gln Gln Cys Gln Arg Arg Cys
 35 40 45

50

Arg Gln Gln Glu Ser Asp Pro Arg Gln Gln Gln Tyr Cys Gln Arg Arg
 50 55 60

Cys Lys Glu Ile Cys Glu Glu Glu Glu Glu Tyr Asn Arg Gln Arg Asp
 65 70 75 80

55

Pro Gln Gln Gln Tyr Glu Gln Cys Gln Lys Arg Cys Gln Arg Arg Glu
 85 90 95

44

	Thr	Glu	Pro	Arg	His	Met	Gln	Ile	Cys	Gln	Gln	Arg	Cys	Glu	Arg	Arg	
				100					105					110			
5	Tyr	Glu	Lys	Glu	Lys	Arg	Lys	Gln	Gln	Lys	Arg	Tyr	Glu	Glu	Gln	Gln	
			115					120					125				
	Arg	Glu	Asp	Glu	Glu	Lys	Tyr	Glu	Glu	Arg	Met	Lys	Glu	Gly	Asp	Asn	
		130					135					140					
10	Lys	Arg	Asp	Pro	Gln	Gln	Arg	Glu	Tyr	Glu	Asp	Cys	Arg	Arg	His	Cys	
	145					150					155					160	
	Glu	Gln	Gln	Glu	Pro	Arg	Leu	Gln	Tyr	Gln	Cys	Gln	Arg	Arg	Cys	Gln	
	165				170					175					180		
15	Glu	Gln	Gln	Arg	Gln	His	Gly	Arg	Gly	Gly	Asp	Leu	Met	Asn	Pro	Gln	
				185					190					195			
	Arg	Gly	Gly	Ser	Gly	Arg	Tyr	Glu	Glu	Gly	Glu	Glu	Lys	Gln	Ser	Asp	
20			200					205						210			
	Asn	Pro	Tyr	Tyr	Phe	Asp	Glu	Arg	Ser	Leu	Ser	Thr	Arg	Phe	Arg	Thr	
		215					220					225					
25	Glu	Glu	Gly	His	Ile	Ser	Val	Leu	Glu	Asn	Phe	Tyr	Gly	Arg	Ser	Lys	
	230					235					240					245	
	Leu	Leu	Arg	Ala	Leu	Lys	Asn	Tyr	Arg	Leu	Val	Leu	Leu	Glu	Ala	Asn	
					250					255					260		
30	Pro	Asn	Ala	Phe	Val	Leu	Pro	Thr	His	Leu	Asp	Ala	Asp	Ala	Ile	Leu	
				265					270					275			
	Leu	Val	Ile	Gly	Gly	Arg	Gly	Ala	Leu	Lys	Met	Ile	His	Arg	Asp	Asn	
35			280					285					290				
	Arg	Glu	Ser	Tyr	Asn	Leu	Glu	Cys	Gly	Asp	Val	Ile	Arg	Ile	Pro	Ala	
		295					300					305					
40	Gly	Thr	Thr	Phe	Tyr	Leu	Ile	Asn	Arg	Asp	Asn	Asn	Glu	Arg	Leu	His	
	310					315					320					325	
	Ile	Ala	Lys	Phe	Leu	Gln	Thr	Ile	Ser	Thr	Pro	Gly	Gln	Tyr	Lys	Glu	
					330					335					340		
45	Phe	Phe	Pro	Ala	Gly	Gly	Gln	Asn	Pro	Glu	Pro	Tyr	Leu	Ser	Thr	Phe	
				345					350					355			
	Ser	Lys	Glu	Ile	Leu	Glu	Ala	Ala	Leu	Asn	Thr	Gln	Thr	Glu	Arg	Leu	
50			360					365					370				
	Arg	Gly	Val	Leu	Gly	Gln	Gln	Arg	Glu	Gly	Val	Ile	Ile	Arg	Ala	Ser	
		375					380					385					
55	Gln	Glu	Gln	Ile	Arg	Glu	Leu	Thr	Arg	Asp	Asp	Ser	Glu	Ser	Arg	Arg	
	390					395					400					405	

45

Trp His Ile Arg Arg Gly Gly Glu Ser Ser Arg Gly Pro Tyr Asn Leu
 410 415 420
 5 Phe Asn Lys Arg Pro Leu Tyr Ser Asn Lys Tyr Gly Gln Ala Tyr Glu
 425 430 435
 Val Lys Pro Glu Asp Tyr Arg Gln Leu Gln Asp Met Asp Val Ser Val
 440 445 450
 10 Phe Ile Ala Asn Ile Thr Gln Gly Ser Met Met Gly Pro Phe Phe Asn
 455 460 470
 Thr Arg Ser Thr Lys Val Val Val Val Ala Ser Gly Glu Ala Asp Val
 15 480 485 490 500
 Glu Met Ala Cys Pro His Leu Ser Gly Arg His Gly Gly Arg Gly Gly
 505 510 515
 20 Gly Lys Arg His Glu Glu Glu Glu Glu Val His Tyr Glu Gln Val Arg
 520 525 530
 Ala Arg Leu Ser Lys Arg Glu Ala Ile Val Val Leu Ala Gly His Pro
 25 535 540 545
 Val Val Phe Val Ser Ser Gly Asn Glu Asn Leu Leu Leu Phe Ala Phe
 550 555 560
 Gly Ile Asn Ala Gln Asn Asn His Glu Asn Phe Leu Ala Gly Arg Glu
 30 565 570 575 580
 Arg Asn Val Leu Gln Gln Ile Glu Pro Gln Ala Met Glu Leu Ala Phe
 585 590 595
 35 Ala Ala Ser Arg Lys Glu Val Glu Glu Leu Phe Asn Ser Gln Asp Glu
 600 605 610
 Ser Ile Phe Phe Pro Gly Pro Arg Gln His Gln Gln Gln Ser Pro Arg
 40 615 620 625
 Ser Thr Lys Gln Gln Gln Pro Leu Val Ser Ile Leu Asp Phe Val Gly
 630 635 640
 Phe

45 (2) INFORMATION FOR SEQ ID NO: 6:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2140 base pairs
 (B) TYPE: nucleic acid
 50 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

 (ii) MOLECULE TYPE: cDNA

 55 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Macadamia integrifolia*

(F) TISSUE TYPE: Seeds

(x) FEATURE:

(A) NAME/KEY: partial mat_peptide

5 (B) LOCATION:1..1875

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

10	CAATGCATGC AGTTAGAGAC ATCAGGCCAG ATGCGTCGGT GTGTGAGTCA GTGCGATAAG	60
	AGATTTGAAG AGGATATAGA TTGGTCTAAG TATGATAACC AAGAGGATCC TCAGACGGAA	120
	TGCCAACAAT GCCAGAGGCG ATGCAGGCAG CAGGAGAGTG ACCCACGTCA GCAACAATAC	180
15	TGCCAACGAC GCTGCAAGGA AATATGTGAA GAAGAAGAAG AATATAACCG ACAACGTGAT	240
	CCACAGCAGC AATACGAGCA ATGTCAGAAG CGCTGCCAAC GGCGCGAGAC AGAGCCACGT	300
20	CACATGCAAA TATGTCAACA ACGCTGCGAG AGGAGATATG AAAAGGAGAA ACGTAAGCAA	360
	CAAAAGAGAT ATGAAGAGCA ACAACGTGAA GACGAAGAGA AATATGAAGA GCGAATGAAG	420
	GAAGGAGATA ACAAACGCGA TCCACAACAA AGAGAGTACG AAGACTGCCG GCGGCACTGC	480
25	GAACAACAGG AGCCACGTCT GCAGTACCAG TGCCAGCGAA GATGCCAAGA GCAGCAGAGG	540
	CAACACGGCC GAGGTGGCGA TTTGATGAAC CCTCAGAGGG GAGGCAGCGG CAGATACGAG	600
30	GAGGGAGAAG AGAAGCAAAG CGACAACCCC TACTACTTCG ACGAACGAAG CTTAAGTACA	660
	AGGTTCAAGG CCGAGGAAGG CCACATCTCA GTTCTGGAGA ACTTCTATGG TAGATCCAAG	720
	CTTCTACGCG CACTAAAAAA CTATCGCTTG GTGCTCCTCG AGGCTAACCC CAACGCCTTC	780
35	GTGCTCCCTA CCCACTTGA TGCAGATGCC ATTCTCTTGG TCATCGGAGG GAGAGGAGCC	840
	CTCAAAATGA TCCACCGTGA CAACAGAGAA TCCTACAACC TCGAGTGTGG AGACGTAATC	900
40	AGAATCCCAG CTGGAACCAC ATTCTACTTA ATCAACCGAG ACAACAACGA GAGGCTCCAC	960
	ATAGCCAAGT TCTTACAGAC CATATCCACT CCTGGCCAAT ACAAGGAATT CTTCCCAGCT	1020
	GGAGGCCAAA ACCCAGAGCC GTACCTCAGT ACCTTCAGCA AAGAGATTCT CGAGGCTGCG	1080
45	CTCAACACAC AAACAGAGAG GCTGCGTGGG GTGCTTGGAC AGCAAAGGGA GGGAGTGATA	1140
	ATTAGGGCGT CACAGGAGCA GATCAGGGAG TTGACTCGAG ATGACTCAGA GTCACGACGC	1200
50	TGGCATATAA GGAGAGGTGG TGAATCAAGC AGGGGACCTT ACAATCTGTT CAACAAAAGG	1260
	CCACTGTACT CCAACAAATA CGGTCAAGCC TACGAAGTCA AACCTGAGGA CTACAGGCAA	1320
	CTCCAAGACA TGGACGTATC AGTTTTTATA GCCAACATCA CCCAGGGATC CATGATGGGT	1380
55	CCCTTCTTCA AACTAGGTC TACAAAGGTG GTAGTGGTGG CTAGTGGAGA GGCAGATGTG	1440

47

GAAATGGCAT GCCCTCACTT GTCGGGAAGA CACGGCGGCC GCGGTGGAGG GAAAAGGCAT 1500
 GAGGAGGAAG AGGAGGTGCA CTATGAGCAG GTTAGAGCAC GTTTGTGCGAA GAGAGAGGCC 1560
 5 ATTGTTGTTC TGGCAGGTCA TCCCGTCGTC TTCGTTTCAT CCGGAAACGA AAACCTGCTG 1620
 CTTTTTGCAT TTGGAATCAA TGCCCAAAAC AACCACGAGA ACTTCCTCGC GGGGAGAGAG 1680
 AGGAACGTGC TGCAGCAGAT AGAGCCACAG GCAATGGAGC TAGCGTTTGC CGCTTCAAGG 1740
 10 AAAGAGGTAG AAGAGTTATT TAACAGCCAG GACGAGTCTA TCTTCTTTCC TGGGCCCAGG 1800
 CAGCACCAGC AACAGTCGCC CCGCTCCACC AAGCAACAAC AGCCTCTCGT CTCCATTCTG 1860
 15 GACTTCGTTG GCTTCTAAAG TTCTACAAAA AAGAGTGTGT TATGTAGTAT AGGTTAGTAG 1920
 CTCCTAGCTC GGTGTATGAG AGTGGTAAGA GACTAAGACG CTAAATCCCT AAGTAACTAA 1980
 CCTGGCGAGC TTGCGTGTAT GCAAATAAAG AGGAACAGCT TTCCAACTTT AGAAAGCTCT 2040
 20 TTTTTTTTTT TTTTTCTTT CTTTTCTTA AGAAATAAAC GAACGTAGAT TGCGGCTCAA 2100
 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 2140

25

(2) INFORMATION FOR SEQ ID NO: 7:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 525 amino acids
 30 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
 35
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Theobroma cacao
 (F) TISSUE TYPE: Seeds

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

Met Val Ile Ser Lys Ser Pro Phe Ile Val Leu Ile Phe Ser Leu Leu
 1 5 10 15
 45 Leu Ser Phe Ala Leu Leu Cys Ser Gly Val Ser Ala Tyr Gly Arg Lys
 20 25 30
 Gln Tyr Glu Arg Asp Pro Arg Gln Gln Tyr Glu Gln Cys Gln Arg Arg
 35 40 45
 50 Cys Glu Ser Glu Ala Thr Glu Glu Arg Glu Gln Glu Gln Cys Glu Gln
 50 55 60
 55 Arg Cys Glu Arg Glu Tyr Lys Glu Gln Gln Arg Gln Gln Glu Glu Glu
 65 70 75 80

48

	Leu	Gln	Arg	Gln	Tyr	Gln	Gln	Cys	Gln	Gly	Arg	Cys	Gln	Glu	Gln	Gln	
					85					90					95		
5	Gln	Gly	Gln	Arg	Glu	Gln	Gln	Gln	Cys	Gln	Arg	Lys	Cys	Trp	Glu	Gln	
				100					105					110			
	Tyr	Lys	Glu	Gln	Glu	Arg	Gly	Glu	His	Glu	Asn	Tyr	His	Asn	His	Lys	
			115					120					125				
10	Lys	Asn	Arg	Ser	Glu	Glu	Glu	Glu	Gly	Gln	Gln	Arg	Asn	Asn	Pro	Tyr	
		130						135				140					
	Tyr	Phe	Pro	Lys	Arg	Arg	Ser	Phe	Gln	Thr	Arg	Phe	Arg	Asp	Glu	Glu	
15		145				150					155				160		
	Gly	Asn	Phe	Lys	Ile	Leu	Gln	Arg	Phe	Ala	Glu	Asn	Ser	Pro	Pro	Leu	
				165						170					175		
20	Lys	Gly	Ile	Asn	Asp	Tyr	Arg	Leu	Ala	Met	Phe	Glu	Ala	Asn	Pro	Asn	
				180					185					190			
	Thr	Phe	Ile	Leu	Pro	His	His	Cys	Asp	Ala	Glu	Ala	Ile	Tyr	Phe	Val	
			195					200					205				
25	Thr	Asn	Gly	Lys	Gly	Thr	Ile	Thr	Phe	Val	Thr	His	Glu	Asn	Lys	Glu	
		210					215					220					
	Ser	Tyr	Asn	Val	Gln	Arg	Gly	Thr	Val	Val	Ser	Val	Pro	Ala	Gly	Ser	
30		225				230					235				240		
	Thr	Val	Tyr	Val	Val	Ser	Gln	Asp	Asn	Gln	Glu	Lys	Leu	Thr	Ile	Ala	
				245						250					255		
35	Val	Leu	Ala	Leu	Pro	Val	Asn	Ser	Pro	Gly	Lys	Tyr	Glu	Leu	Phe	Phe	
			260						265					270			
	Pro	Ala	Gly	Asn	Asn	Lys	Pro	Glu	Ser	Tyr	Tyr	Gly	Ala	Phe	Ser	Tyr	
			275					280					285				
40	Glu	Val	Leu	Glu	Thr	Val	Phe	Asn	Thr	Gln	Arg	Glu	Lys	Leu	Glu	Glu	
		290					295					300					
	Ile	Leu	Glu	Glu	Gln	Arg	Gly	Gln	Lys	Arg	Gln	Gln	Gly	Gln	Gln	Gly	
45		305				310					315				320		
	Met	Phe	Arg	Lys	Ala	Lys	Pro	Glu	Gln	Ile	Arg	Ala	Ile	Ser	Gln	Gln	
				325						330					335		
50	Ala	Thr	Ser	Pro	Arg	His	Arg	Gly	Gly	Glu	Arg	Leu	Ala	Ile	Asn	Leu	
				340					345					350			
	Leu	Ser	Gln	Ser	Pro	Val	Tyr	Ser	Asn	Gln	Asn	Gly	Arg	Phe	Phe	Glu	
			355					360					365				
55	Ala	Cys	Pro	Glu	Asp	Phe	Ser	Gln	Phe	Gln	Asn	Met	Asp	Val	Ala	Val	
		370					375					380					

Ser Ala Phe Lys Leu Asn Gln Gly Ala Ile Phe Val Pro His Tyr Asn
 385 390 395 400
 5 Ser Lys Ala Thr Phe Val Val Phe Val Thr Asp Gly Tyr Gly Tyr Ala
 405 410 415
 Gln Met Ala Cys Pro His Leu Ser Arg Gln Ser Gln Gly Ser Gln Ser
 420 425 430
 10 Gly Arg Gln Asp Arg Arg Glu Gln Glu Glu Ser Glu Glu Glu Thr
 435 440 445
 Phe Gly Glu Phe Gln Gln Val Lys Ala Pro Leu Ser Pro Gly Asp Val
 450 455 460
 15 Phe Val Ala Pro Ala Gly His Ala Val Thr Phe Phe Ala Ser Lys Asp
 465 470 475 480
 Gln Pro Leu Asn Ala Val Ala Phe Gly Leu Asn Ala Gln Asn Asn Gln
 485 490 495
 20 Arg Ile Phe Leu Ala Gly Arg Pro Phe Phe Leu Asn His Lys Gln Asn
 500 505 510
 25 Thr Asn Val Ile Lys Phe Thr Val Lys Ala Ser Ala Tyr
 515 520 525

30 (2) INFORMATION FOR SEQ ID NO: 8:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 590 amino acids
 (B) TYPE: amino acid
 35 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: protein
 40 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Gossypium hirsutum*
 (F) TISSUE TYPE: Seeds
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

45 Met Val Arg Asn Lys Ser Ala Cys Val Val Leu Leu Phe Ser Leu Phe
 1 5 10 15
 50 Leu Ser Phe Gly Leu Leu Cys Ser Ala Lys Asp Phe Pro Gly Arg Arg
 20 25 30
 Gly Asp Asp Asp Pro Pro Lys Arg Tyr Glu Asp Cys Arg Arg Arg Cys
 35 40 45
 55 Glu Trp Asp Thr Arg Gly Gln Lys Glu Gln Gln Gln Cys Glu Glu Ser
 50 55 60

	Cys	Lys	Ser	Gln	Tyr	Gly	Glu	Lys	Asp	Gln	Gln	Gln	Arg	His	Arg	Pro
	65					70					75					80
5	Glu	Asp	Pro	Gln	Arg	Arg	Tyr	Glu	Glu	Cys	Gln	Gln	Glu	Cys	Arg	Gln
					85					90					95	
	Gln	Glu	Glu	Arg	Gln	Gln	Pro	Gln	Cys	Gln	Gln	Arg	Cys	Leu	Lys	Arg
10				100					105					110		
	Phe	Glu	Gln	Glu	Gln	Gln	Gln	Ser	Gln	Arg	Gln	Phe	Gln	Glu	Cys	Gln
		115						120					125			
15	Gln	His	Cys	His	Gln	Gln	Glu	Gln	Arg	Pro	Glu	Lys	Lys	Gln	Gln	Cys
	130						135					140				
	Val	Arg	Glu	Cys	Arg	Glu	Lys	Tyr	Gln	Glu	Asn	Pro	Trp	Arg	Gly	Glu
	145					150					155					160
20	Arg	Glu	Glu	Glu	Ala	Glu	Glu	Glu	Glu	Thr	Glu	Glu	Gly	Glu	Gln	Glu
					165					170					175	
	Gln	Ser	His	Asn	Pro	Phe	His	Phe	His	Arg	Arg	Ser	Phe	Gln	Ser	Arg
25				180					185					190		
	Phe	Arg	Glu	Glu	His	Gly	Asn	Phe	Arg	Val	Leu	Gln	Arg	Phe	Ala	Ser
		195						200					205			
30	Arg	His	Pro	Ile	Leu	Arg	Gly	Ile	Asn	Glu	Phe	Arg	Leu	Ser	Ile	Leu
	210						215					220				
	Glu	Ala	Asn	Pro	Asn	Thr	Phe	Val	Leu	Pro	His	His	Cys	Asp	Ala	Glu
	225					230					235					240
35	Lys	Ile	Tyr	Leu	Val	Thr	Asn	Gly	Arg	Gly	Thr	Leu	Thr	Phe	Leu	Thr
				245						250					255	
	His	Glu	Asn	Lys	Glu	Ser	Tyr	Asn	Ile	Val	Pro	Gly	Val	Val	Val	Lys
40				260					265					270		
	Val	Pro	Ala	Gly	Ser	Thr	Val	Tyr	Leu	Ala	Asn	Gln	Asp	Asn	Lys	Glu
		275						280					285			
45	Lys	Leu	Ile	Ile	Ala	Val	Leu	His	Arg	Pro	Val	Asn	Asn	Pro	Gly	Gln
	290						295					300				
	Phe	Glu	Glu	Phe	Phe	Pro	Ala	Gly	Ser	Gln	Arg	Pro	Gln	Ser	Tyr	Leu
	305					310					315					320
50	Arg	Ala	Phe	Ser	Arg	Glu	Ile	Leu	Glu	Pro	Ala	Phe	Asn	Thr	Arg	Ser
					325					330					335	
	Glu	Gln	Leu	Asp	Glu	Leu	Phe	Gly	Gly	Arg	Gln	Ser	Arg	Arg	Arg	Gln
55				340					345					350		
	Gln	Gly	Gln	Gly	Met	Phe	Arg	Lys	Ala	Ser	Gln	Glu	Gln	Ile	Arg	Ala

51

	355		360		365
	Leu Ser Gln Glu Ala Thr Ser Pro Arg Glu Lys Ser Gly Glu Arg Phe				
	370		375		380
5	Ala Phe Asn Leu Leu Ser Gln Thr Pro Arg Tyr Ser Asn Gln Asn Gly				
	385		390		395 400
10	Arg Phe Phe Glu Ala Cys Pro Pro Glu Phe Arg Gln Leu Arg Asp Ile				
		405		410	415
	Asn Val Thr Val Ser Ala Leu Gln Leu Asn Gln Gly Ser Ile Phe Val				
		420		425	430
15	Pro His Tyr Asn Ser Lys Ala Thr Phe Val Ile Leu Val Thr Glu Gly				
		435		440	445
	Asn Gly Tyr Ala Glu Met Val Ser Pro His Leu Pro Arg Gln Ser Ser				
20		450		455	460
	Tyr Glu Glu Glu Glu Glu Glu Asp Glu Glu Glu Glu Gln Glu Gln Glu				
	465		470		475 480
25	Glu Glu Arg Arg Ser Gly Gln Tyr Arg Lys Ile Arg Ser Arg Leu Ser				
		485		490	495
	Arg Gly Asp Ile Phe Val Val Pro Ala Asn Phe Pro Val Thr Phe Val				
		500		505	510
30	Ala Ser Gln Asn Gln Asn Leu Arg Met Thr Gly Phe Gly Leu Tyr Asn				
		515		520	525
	Gln Asn Ile Asn Pro Asp His Asn Gln Arg Ile Phe Val Ala Gly Lys				
35		530		535	540
	Ile Asn His Val Arg Gln Trp Asp Ser Gln Ala Lys Glu Leu Ala Phe				
	545		550		555 560
40	Gly Val Ser Ser Arg Leu Val Asp Glu Ile Phe Asn Ser Asn Pro Gln				
		565		570	575
	Glu Ser Tyr Phe Val Ser Arg Gln Arg Gln Arg Ala Ser Glu				
		580		585	590

45 (2) INFORMATION FOR SEQ ID NO: 9:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 22 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

50

(ii) MOLECULE TYPE: protein

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

52

Arg Gln Arg Asp Pro Gln Gln Gln Ala Glu Gln Ala Gln Lys Arg Ala
 1 5 10 15

Gln Arg Arg Glu Thr Glu
 20

5

(2) INFORMATION FOR SEQ ID NO: 10:

10

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

15

- (ii) MOLECULE TYPE: protein

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

20

Pro Arg His Met Gln Ile Ala Gln Gln Arg Ala Glu Arg Arg Ala Glu
 1 5 10 15

Lys Glu Lys Arg Lys Gln Gln Lys Arg
 20 25

25

(2) INFORMATION FOR SEQ ID NO: 11:

30

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 30 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

35

- (ii) MOLECULE TYPE: protein

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

40

Met Ala Trp Phe His Val Ser Val Cys Asn Ala Val Phe Val Val Ile
 1 5 10 15

Ile Ile Ile Met Leu Leu Met Phe Val Pro Val Val Arg Gly
 20 25 30

45

(2) INFORMATION FOR SEQ ID NO: 12:

50

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleotide
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

55

- (ii) MOLECULE TYPE: nucleotide

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

CAGCAGCAGT ATGAGCAGTG

20

5 (2) INFORMATION FOR SEQ ID NO: 13:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 base pairs
 (B) TYPE: nucleic acid
10 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

TTTTTCGTAK CKKCKTTCGC A

21

20 (2) INFORMATION FOR SEQ ID NO: 14:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 base pairs
 (B) TYPE: nucleic acid
25 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

ACACCATATG CGACAACGTG ATCC

24

35 (2) INFORMATION FOR SEQ ID NO: 15:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 26 base pairs
 (B) TYPE: nucleic acid
40 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

CGTTGTTTTTC TCTATTCCTA GGGTTG

26

50 (2) INFORMATION FOR SEQ ID NO: 16:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 amino acids
 (B) TYPE: amino acid
55 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

5

Met Gly His His His His His His His His His His Ser Ser Gly His
1 5 10 15

10

Ile Glu Gly Arg His Met
20

(2) INFORMATION FOR SEQ ID NO: 17:

15

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 90 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17

25

GGGAATTCCA TATGTATGAG CGTGATCCTC GACAGCAATA CGAGCAATGC CAGAGGCGAT 60
GCGAGTCGGA AGCGACTGAA GAAAGGGAGC 90

30

(2) INFORMATION FOR SEQ ID NO: 18

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 91 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

35

(ii) MOLECULE TYPE: DNA

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

GAAGCGACTG AAGAAAGGGA GCAAGAGCAG TGTGAACAAC GCTGTGAAAG GGAGTACAAG 60
GAGCAGCAGA GACAGCAATA GGGATCCACA C 91

45

(2) INFORMATION FOR SEQ ID NO: 19

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 101 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

50

55

(ii) MOLECULE TYPE: DNA

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

GGGAATTCCA TATGCTTCAA AGGCAATACC AGCAATGTCA AGGGCGTTGT CAAGAGCAAC 60
 5 AACAGGGGCA GAGAGAGCAG CAGCAGTGCC AGAGAAAATG C 101

(2) INFORMATION FOR SEQ ID NO: 20

10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 102 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 15 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20

20 GTGTGGATCC CTAGCTCCTA TTTTTTTTGT GATTATGGTA ATTCTCGTGC TCGCCTCTCT 60
 CTTGTTTCCTT ATATTGCTCC CAGCATTTTC TCTGGCACTG CT 102

25

(2) INFORMATION FOR SEQ ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 42 amino acids
 30 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

35

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Peanut
 (F) TISSUE TYPE: Seeds

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

Met Arg Gly Arg Val Ser Pro Leu Met Leu Leu Leu Gly Ile Leu Val
 1 5 10 15
 45 Leu Ala Ser Val Ser Ala Thr Gln Ala Lys Ser Pro Tyr Arg Lys Thr
 20 25 30
 Glu Asn Pro Cys Ala Gln Arg Cys Leu Gln Ser Cys Gln Gln Glu Pro
 35 40 45
 50 Asp Asp Leu Lys Gln Lys Ala Cys Glu Ser Arg Cys Thr Lys Leu Glu
 50 55 60
 55 Tyr Asp Pro Arg Cys Val Tyr Asp Thr Gly Ala Thr Asn Gln Arg His
 65 70 75 80

56

	Pro	Pro	Gly	Glu	Arg	Thr	Arg	Gly	Arg	Gln	Pro	Gly	Asp	Tyr	Asp	Asp	
	85										90			95			
5	Asp	Arg	Arg	Gln	Pro	Arg	Arg	Glu	Glu	Gly	Gly	Arg	Trp	Gly	Pro	Ala	
				100						105			110				
	Glu	Pro	Arg	Glu	Arg	Glu	Arg	Glu	Glu	Asp	Trp	Arg	Gln	Pro	Arg	Glu	
				115						120			125				
10	Asp	Trp	Arg	Arg	Pro	Ser	His	Gln	Gln	Pro	Arg	Lys	Ile	Arg	Pro	Glu	
				130									140				
	Gly	Arg	Glu	Gly	Glu	Gln	Glu	Trp	Gly	Thr	Pro	Gly	Ser	Glu	Val	Arg	
				145						150			155				
15	Glu	Glu	Thr	Ser	Arg	Asn	Asn	Pro	Phe	Tyr	Phe	Pro	Ser	Arg	Arg	Phe	
				165						170			175				
										180							
20	Ser	Thr	Arg	Tyr	Gly	Asn	Gln	Asn	Gly	Arg	Ile	Arg	Val	Leu	Gln	Arg	
				185						190			195				
	Phe	Asp	Gln	Arg	Ser	Lys	Gln	Phe	Gln	Asn	Leu	Gln	Asn	His	Arg	Ile	
				200						205			210				
25	Val	Gln	Ile	Glu	Ala	Arg	Pro	Asn	Thr	Leu	Val	Leu	Pro	Lys	His	Ala	
				215						220			225				
	Asp	Ala	Asp	Asn	Ile	Leu	Val	Ile	Gln	Gln	Gly	Gln	Ala	Thr	Val	Thr	
				230						235			240				
30	Val	Ala	Asn	Gly	Asn	Asn	Arg	Lys	Ser	Phe	Asn	Leu	Asp	Glu	Gly	His	
							250			255			260				
	Ala	Leu	Arg	Ile	Pro	Ser	Gly	Phe	Ile	Ser	Tyr	Ile	Leu	Asn	Arg	His	
				265						270			275				
	Asp	Asn	Gln	Asn	Leu	Arg	Val	Ala	Lys	Ile	Ser	Met	Pro	Val	Asn	Thr	
				280						285			290				
40	Pro	Gly	Gln	Phe	Glu	Asp	Phe	Phe	Pro	Ala	Ser	Ser	Arg	Asp	Gln	Ser	
				295						300			305				
	Ser	Tyr	Leu	Gln	Gly	Phe	Ser	Arg	Asn	Thr	Leu	Glu	Ala	Ala	Phe	Asn	
				310						315			320				
45	Ala	Glu	Phe	Asn	Glu	Ile	Arg	Arg	Val	Leu	Leu	Glu	Glu	Asn	Ala	Gly	
							330			335			340				
	Gly	Glu	Gln	Glu	Glu	Arg	Gly	Gln	Arg	Arg	Arg	Ser	Thr	Arg	Ser	Ser	
				345								350			355		
50	Asp	Asn	Glu	Gly	Val	Ile	Val	Lys	Val	Ser	Lys	Glu	His	Val	Gln	Glu	
				360								365			370		
55	Leu	Thr	Lys	His	Ala	Lys	Ser	Val	Ser	Lys	Lys	Gly	Ser	Glu	Glu	Glu	
				375								380			385		

Asp Ile Thr Asn Pro Ile Asn Leu Arg Asp Gly Glu Pro Asp Leu Ser
 390 395 400 405
 5 Asn Asn Phe Gly Arg Leu Phe Glu Val Lys Pro Asp Lys Lys Asn Pro
 410 415 420
 Gln Leu Gln Asp Leu Asp Met Met Leu Thr Cys Val Glu Ile Lys Glu
 425 430 435
 10 Gly Ala Leu Met Leu Pro His Phe Asn Ser Lys Ala Met Val Ile Val
 440 445 450
 Val Val Asn Lys Gly Thr Gly Asn Leu Glu Leu Val Ala Val Arg Lys
 15 455 460 470
 Glu Gln Gln Gln Arg Gly Arg Arg Glu Gln Glu Trp Glu Glu Glu Glu
 480 485 490 500
 20 Glu Asp Glu Glu Glu Glu Gly Ser Asn Arg Glu Val Arg Arg Tyr Thr
 505 510 515
 Ala Arg Leu Lys Glu Gly Asp Val Phe Ile Met Pro Ala Ala His Pro
 520 525 530
 25 Val Ala Ile Asn Ala Ser Ser Glu Leu His Leu Leu Gly Phe Gly Ile
 535 540 545
 Asn Ala Glu Asn Asn His Arg Ile Phe Leu Ala Gly Asp Lys Asp Asn
 30 550 555 560
 Val Ile Asp Gln Ile Glu Lys Gln Ala Lys Asp Leu Ala Phe Pro Gly
 565 570 575 580
 35 Ser Gly Glu Gln Val Glu Lys Leu Ile Lys Asn Gln Arg Glu Ser His
 585 590 595
 Phe Val Ser Ala Arg Pro Gln Ser Gln Ser Pro Ser Ser Pro Glu Lys
 600 605 610
 40 Glu Asp Gln Glu Glu Glu Asn Gln Gly Gly Lys Gly Pro Leu Leu Ser
 615 620 625
 Ile Leu Lys Ala Phe Asn
 45 630

(2) INFORMATION FOR SEQ ID NO: 22:

- 50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 46 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 55 (ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Maize
 (F) TISSUE TYPE: Seeds

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

Met Val Ser Ala Arg Ile Val Val Leu Leu Ala Thr Leu Leu Cys Ala
 1 5 10 15

Ala Ala Ala Val Ala Ser Ser Trp Glu Asp Asp Asn His His His His
 20 25 30

Gly Gly His Lys Ser Gly Gln Cys Val Arg Arg Cys Glu Asp Arg Pro
 35 40 45

Trp His Gln Arg Pro Arg Cys Leu Glu Gln Cys Arg Glu Glu Glu Arg
 50 55 60

Glu Lys Arg Gln Glu Arg Ser Arg His Glu Ala Asp Asp Arg Ser Gly
 65 70 75 80

Glu Gly Ser Ser Glu Asp Glu Arg Glu Gln Glu Lys Glu Lys Gln Lys
 85 90 95

Asp Arg Arg Pro Tyr Val Phe Asp Arg Arg Ser Phe Arg Arg Val Val
 100 105 110

Arg Ser Glu Gln Gly Ser Leu Arg Val Leu Arg Pro Phe Asp Glu Val
 115 120 125

Ser Arg Leu Leu Arg Gly Ile Arg Asp Tyr Arg Val Ala Val Leu Glu
 130 135 140

Ala Asn Pro Arg Ser Phe Val Val Pro Ser His Thr Asp Ala His Cys
 145 150 155 160

Ile Cys Tyr Val Ala Glu Gly Glu Gly Val Val Thr Thr Ile Glu Asn
 165 170 175 180

Gly Glu Arg Arg Ser Tyr Thr Ile Lys Gln Gly His Val Phe Val Ala
 185 190 195

Pro Ala Gly Ala Val Thr Tyr Leu Ala Asn Thr Asp Gly Arg Lys Lys
 200 205 210

Leu Val Ile Thr Lys Ile Leu His Thr Ile Ser Val Pro Gly Glu Phe
 215 220 225

Gln Phe Phe Phe Gly Pro Gly Gly Arg Asn Pro Glu Ser Phe Leu Ser
 230 235 240 245

Ser Phe Ser Lys Ser Ile Gln Arg Ala Ala Tyr Lys Thr Ser Ser Asp
 250 255 260

Arg Leu Glu Arg Leu Phe Gly Arg His Gly Gln Asp Lys Gly Ile Ile

	265	270	275
	Val Arg Ala Thr Glu Glu Gln Thr Arg Glu Leu Arg Arg His Ala Ser		
	280	285	290
5	Glu Gly Gly His Gly Pro His Trp Pro Leu Pro Pro Phe Gly Glu Ser		
	295	300	305
10	Arg Gly Pro Tyr Ser Leu Leu Asp Gln Arg Pro Ser Ile Ala Asn Gln		
	310	315	320 325
	His Gly Gln Leu Tyr Glu Ala Asp Ala Arg Ser Phe His Asp Leu Ala		
	330	335	340
15	Glu His Asp Val Ser Val Ser Phe Ala Asn Ile Thr Ala Gly Ser Met		
	345	350	355
	Ser Ala Pro Leu Phe Asn Thr Arg Ser Phe Lys Ile Ala Tyr Val Pro		
20	360	365	370
	Asn Gly Lys Gly Tyr Ala Glu Ile Val Cys Pro His Arg Gln Ser Gln		
	375	380	385
25	Gly Gly Glu Ser Glu Arg Glu Arg Asp Lys Gly Arg Arg Ser Glu Glu		
	390	395	400 405
	Glu Glu Glu Glu Ser Ser Glu Glu Gln Glu Glu Ala Gly Gln Gly Tyr		
	410	415	420
30	His Thr Ile Arg Ala Arg Leu Ser Pro Gly Thr Ala Phe Val Val Pro		
	425	430	435
	Ala Gly His Pro Phe Val Ala Val Ala Ser Arg Asp Ser Asn Leu Gln		
35	440	445	450
	Ile Val Cys Phe Glu Val His Ala Asp Arg Asn Glu Lys Val Phe Leu		
	455	460	470
40	Ala Gly Ala Asp Asn Val Leu Gln Lys Leu Asp Arg Val Ala Lys Ala		
	480	485	490 500
	Leu Ser Phe Ala Ser Lys Ala Glu Glu Val Asp Glu Val Leu Gly Ser		
	505	510	515
45	Arg Arg Glu Lys Gly Phe Leu Pro Gly Pro Glu Glu Ser Gly Gly His		
	520	525	530
	Glu Glu Arg Glu Gln Glu Glu Glu Glu Arg Glu Glu Arg His Gly Gly		
50	535	540	545
	Arg Gly Glu Arg Glu Arg His Gly Arg Glu Glu Arg Glu Lys Glu Glu		
	550	555	560
55	Glu Arg Glu Gly Arg His Gly Gly Arg Glu Glu Arg Glu Glu Glu Glu		
	565	570	575 580

60

Arg His Gly Arg Gly Arg Arg Glu Glu Val Ala Glu Thr Leu Met Arg
585 590 595

Met Val Thr Ala Arg Met
5 600

(2) INFORMATION FOR SEQ ID NO: 23:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Maize
20 (F) TISSUE TYPE: Seeds

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

25 Arg Ser Gly Arg Gly Glu Cys Arg Arg Gln Cys Leu Arg Arg His Glu
1 5 10 15

Gly Gln Pro Trp Glu Thr Gln Glu Cys Met Arg Arg Cys Arg Arg Arg
20 25 30

30 Gly

(2) INFORMATION FOR SEQ ID NO: 24:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 42 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Barley
45 (F) TISSUE TYPE: Seeds

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

50 Met Ala Thr Arg Ala Lys Ala Thr Ile Pro Leu Leu Phe Leu Leu Gly
1 5 10 15

Thr Ser Leu Leu Phe Ala Ala Ala Val Ser Ala Ser His Asp Asp Glu
20 25 30

55 Asp Asp Arg Arg Gly Gly His Ser Leu Gln Gln Cys Val Gln Arg Cys
 35 40 45

Arg Gln Glu Arg Pro Arg Tyr Ser His Ala Arg Cys Val Gln Glu Cys
 50 55 60

5 Arg Asp Asp Gln Gln Gln His Gly Arg His Glu Gln Glu Glu Glu Gln
 65 70 75 80

Gly Arg Gly Arg Gly Trp His Gly Glu Gly Glu Arg Glu Glu Glu His
 85 90 95

10 Gly Arg Gly Arg Gly Arg His Gly Glu Gly Glu Arg Glu Glu Glu His
 100 105 110

Gly Arg Gly Arg Gly Arg His Gly Glu Gly Glu Arg Glu Glu Glu Arg
 115 120 125

15 Gly Arg Gly His Gly Arg His Gly Glu Gly Glu Arg Glu Glu Glu Arg
 130 135 140

20 Gly Arg Gly Arg Gly Arg His Gly Glu Gly Glu Arg Glu Glu Glu Glu
 145 150 155 160

Gly Arg Gly Arg Gly Arg Arg Gly Glu Gly Glu Arg Asp Glu Glu Gln
 165 170 175 180

25 Gly Asp Ser Arg Arg Pro Tyr Val Phe Gly Pro Arg Ser Phe Arg Arg
 185 190 195

30 Ile Ile Gln Ser Asp His Gly Phe Val Arg Ala Leu Arg Pro Phe Asp
 200 205 210

Gln Val Ser Arg Leu Leu Arg Gly Ile Arg Asp Tyr Arg Val Ala Ile
 215 220 225

35 Met Glu Val Asn Pro Arg Ala Phe Val Val Pro Gly Phe Thr Asp Ala
 230 235 240 245

Asp Gly Val Gly Tyr Val Ala Gln Gly Glu Gly Val Leu Thr Val Ile
 250 255 260

40 Glu Asn Gly Glu Lys Arg Ser Tyr Thr Val Lys Glu Gly Asp Val Ile
 265 270 275

Val Ala Pro Ala Gly Ser Ile Met His Leu Ala Asn Thr Asp Gly Arg
 280 285 290

Arg Lys Leu Val Ile Ala Lys Ile Leu His Thr Ile Ser Val Pro Gly
 295 300 305

50 Lys Phe Gln Phe Leu Ser Val Lys Pro Leu Leu Ala Ser Leu Ser Lys
 310 315 320 325

Arg Val Leu Arg Ala Ala Phe Lys Thr Ser Asp Glu Arg Leu Glu Arg
 330 335 340

55 Leu Phe Asn Gln Arg Gln Gly Gln Glu Lys Thr Arg Ser Val Ser Ile

62

		345		350		355										
	Val	Arg	Ala	Ser	Glu	Glu	Gln	Leu	Arg	Glu	Leu	Arg	Arg	Glu	Ala	Ala
		360						365					370			
5	Glu	Gly	Gly	Gln	Gly	His	Arg	Trp	Pro	Leu	Pro	Pro	Phe	Arg	Gly	Asp
		375					380						385			
10	Ser	Arg	Asp	Thr	Phe	Asn	Leu	Leu	Glu	Gln	Arg	Pro	Lys	Ile	Ala	Asn
	390					395					400					405
	Arg	His	Gly	Arg	Leu	Tyr	Glu	Ala	Asp	Ala	Arg	Ser	Phe	His	Ala	Leu
					410					415					420	
15	Ala	Asn	Gln	Asp	Val	Arg	Val	Ala	Val	Ala	Asn	Ile	Thr	Pro	Gly	Ser
				425					430						435	
20	Met	Thr	Ala	Pro	Tyr	Leu	Asn	Thr	Gln	Ser	Phe	Lys	Leu	Ala	Val	Val
			440					445					450			
	Leu	Glu	Gly	Glu	Gly	Glu	Val	Gln	Ile	Val	Cys	Pro	His	Leu	Gly	Arg
		455					460					470				
25	Glu	Ser	Glu	Ser	Glu	Arg	Glu	His	Gly	Lys	Gly	Arg	Arg	Arg	Glu	Glu
	480					485					490					500
	Glu	Glu	Asp	Asp	Gln	Arg	Gln	Gln	Arg	Arg	Arg	Gly	Ser	Glu	Ser	Glu
					505				510						515	
30	Ser	Glu	Glu	Glu	Glu	Gln	Gln	Arg	Tyr	Glu	Thr	Val	Arg	Ala	Arg	
				520				525					530			
	Val	Ser	Arg	Gly	Ser	Ala	Phe	Val	Val	Pro	Pro	Gly	His	Pro	Val	Val
			535					540					545			
35	Glu	Ile	Ser	Ser	Ser	Gln	Gly	Ser	Ser	Asn	Leu	Gln	Val	Val	Cys	Phe
		550					555					560				
40	Glu	Ile	Asn	Ala	Glu	Arg	Asn	Glu	Arg	Val	Trp	Leu	Ala	Gly	Arg	Asn
	565					570				575						580
	Asn	Val	Ile	Gly	Lys	Leu	Gly	Ser	Pro	Ala	Gln	Glu	Leu	Thr	Phe	Gly
					585					590					595	
45	Arg	Pro	Ala	Arg	Glu	Val	Gln	Glu	Val	Phe	Arg	Ala	Gln	Asp	Gln	Asp
			600						605					610		
	Glu	Gly	Phe	Val	Ala	Gly	Pro	Glu	Gln	Gln	Ser	Arg	Glu	Gln	Glu	Gln
			615					620					625			
50	Glu	Gln	Glu	Arg	His	Arg	Arg	Arg	Gly	Asp	Arg	Gly	Arg	Gly	Asp	Glu
		630					635					640				
55	Ala	Val	Glu	Thr	Phe	Leu	Arg	Met	Ala	Thr	Gly	Ala	Ile			
	645					650					655					

(2) INFORMATION FOR SEQ ID NO: 25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Soybean (Glycine max)
 (F) TISSUE TYPE: Seeds

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

```

Met Met Arg Ala Arg Phe Pro Leu Leu Leu Gly Leu Val Phe Leu
1           5           10           15
Ala Ser Val Ser Val Ser Phe Gly Ile Ala Tyr Trp Glu Lys Glu Asn
20          20          25          30
Pro Lys His Asn Lys Cys Leu Gln Ser Cys Asn Ser Glu Arg Asp Ser
25          35          40          45
Tyr Arg Asn Gln Ala Cys His Ala Arg Cys Asn Leu Leu Lys Val Glu
50          55          60
Lys Glu Glu Cys Glu Glu Gly Glu Ile Pro Arg Pro Arg Pro Arg Pro
30          65          70          75          80
Gln His Pro Glu Arg Glu Pro Gln Gln Pro Gly Glu Lys Glu Glu Asp
35          85          90          95
Glu Asp Glu Gln Pro Arg Pro Ile Pro Phe Pro Arg Pro Gln Pro Arg
100         105         110
Gln Glu Glu Glu His Glu Gln Arg Glu Glu Gln Glu Trp Pro Arg Lys
40         115         120         125
Glu Glu Lys Arg Gly Glu Lys Gly Ser Glu Glu Glu Asp Glu Asp Glu
130         135         140
Asp Glu Glu Gln Asp Glu Arg Gln Phe Pro Phe Pro Arg Pro Pro His
45         145         150         155         160
Gln Lys Glu Glu Arg Asn Glu Glu Glu Asp Glu Asp Glu Glu Gln Gln
50         165         170         175         180
Arg Glu Ser Glu Glu Ser Glu Asp Ser Glu Leu Arg Arg His Lys Asn
185         190         195
Lys Asn Pro Phe Leu Phe Gly Ser Asn Arg Phe Glu Thr Leu Phe Lys
55         200         205         210

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	Asn	Gln	Tyr	Gly	Arg	Ile	Arg	Val	Leu	Gln	Arg	Phe	Asn	Gln	Arg	Ser	
	215						220					225					
5	Pro	Gln	Leu	Gln	Asn	Leu	Arg	Asp	Tyr	Arg	Ile	Leu	Glu	Phe	Asn	Ser	
	230				235					240						245	
	Lys	Pro	Asn	Thr	Leu	Leu	Leu	Pro	Asn	His	Ala	Asp	Ala	Asp	Tyr	Leu	
					250				255						260		
10	Ile	Val	Ile	Leu	Asn	Gly	Thr	Ala	Ile	Leu	Ser	Leu	Val	Asn	Asn	Asp	
				265				270						275			
	Asp	Arg	Asp	Ser	Tyr	Arg	Leu	Gln	Ser	Gly	Asp	Ala	Leu	Arg	Val	Pro	
15			280					285					290				
	Ser	Gly	Thr	Thr	Tyr	Tyr	Val	Val	Asn	Pro	Asp	Asn	Asn	Glu	Asn	Leu	
		295					300				305						
20	Arg	Leu	Ile	Thr	Leu	Ala	Ile	Pro	Val	Asn	Lys	Pro	Gly	Arg	Phe	Glu	
	310				315					320						325	
	Ser	Phe	Phe	Leu	Ser	Ser	Thr	Glu	Ala	Gln	Gln	Ser	Tyr	Leu	Gln	Gly	
				330				335							340		
25	Phe	Ser	Arg	Asn	Ile	Leu	Glu	Ala	Ser	Tyr	Asp	Thr	Lys	Phe	Glu	Glu	
				345				350						355			
	Ile	Asn	Lys	Val	Leu	Phe	Ser	Arg	Glu	Glu	Gly	Gln	Gln	Gln	Gly	Glu	
30			360					365				370					
	Gln	Arg	Leu	Gln	Glu	Ser	Val	Ile	Val	Glu	Ile	Ser	Lys	Glu	Gln	Ile	
		375				380					385						
35	Arg	Ala	Leu	Ser	Lys	Arg	Ala	Lys	Ser	Ser	Ser	Arg	Lys	Thr	Ile	Ser	
	390				395						400					405	
	Ser	Glu	Asp	Lys	Pro	Phe	Asn	Leu	Arg	Ser	Arg	Asp	Pro	Ile	Tyr	Ser	
				410					415					420			
40	Asn	Lys	Leu	Gly	Lys	Phe	Phe	Glu	Ile	Thr	Pro	Glu	Lys	Asn	Pro	Gln	
			425					430						435			
	Leu	Arg	Asp	Leu	Asp	Ile	Phe	Leu	Ser	Ile	Val	Asp	Met	Asn	Glu	Gly	
45			440				445					450					
	Ala	Leu	Leu	Leu	Pro	His	Phe	Asn	Ser	Lys	Ala	Ile	Val	Ile	Leu	Val	
		455				460					470						
50	Ile	Asn	Glu	Gly	Asp	Ala	Asn	Ile	Glu	Leu	Val	Gly	Leu	Lys	Glu	Gln	
	480				485				490						500		
	Gln	Gln	Glu	Gln	Gln	Gln	Glu	Glu	Gln	Pro	Leu	Glu	Val	Arg	Lys	Tyr	
				505					510					515			
55	Arg	Ala	Glu	Leu	Ser	Glu	Gln	Asp	Ile	Phe	Val	Ile	Pro	Ala	Gly	Tyr	
			520					525					530				

Pro Val Val Val Asn Ala Thr Ser Asn Leu Asn Phe Phe Ala Ile Gly
 535 540 545

5 Ile Asn Ala Glu Asn Asn Gln Arg Asn Phe Leu Ala Gly Ser Gln Asp
 550 555 560

Asn Val Ile Ser Gln Ile Pro Ser Gln Val Gln Glu Leu Ala Phe Pro
 565 570 575 580

10 Gly Ser Ala Gln Ala Val Glu Lys Leu Leu Lys Asn Gln Arg Glu Ser
 585 590 595

15 Tyr Phe Val Asp Ala Gln Pro Lys Lys Lys Glu Glu Gly Asn Lys Gly
 600 605 610

Arg Lys Gly Pro Leu Ser Ser Ile Leu Arg Ala Phe Tyr
 615 620 625

20

(2) INFORMATION FOR SEQ ID NO: 26:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

25

(ii) MOLECULE TYPE: protein

30

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Stenocarpus sinuatus*
 (F) TISSUE TYPE: Seeds

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

Val Lys Glu Asp His Gln Phe Glu Thr Arg Gly Glu Ile Leu Glu Cys
 1 5 10 15

40 Tyr Arg Leu Cys Gln Gln Gln
 20

(28) INFORMATION FOR SEQ ID NO: 27:

45

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

50

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Stenocarpus sinuatus*
 (F) TISSUE TYPE: Seeds

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

5 Gln Lys His Arg Ser Gln Ile Leu Gly Cys Tyr Leu Xxx cys Gln Gln
1 5 10 15
Leu

10 (2) INFORMATION FOR SEQ ID NO: 28:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 28 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

20 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Stenocarpus sinuatus*
(F) TISSUE TYPE: Seeds

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

Leu Asp Pro Ile Arg Gln Gln Gln Leu Cys Gln Met Arg Cys Gln Gln
1 5 10 15
Gln Glu Lys Asp Pro Arg Gln Gln Gln Gln Cys Lys
20 25

CLAIMS

1. A protein fragment having antimicrobial activity, wherein said protein fragment is selected from:

(ii) a polypeptide having an amino acid sequence selected from:

- 5 residues 29 to 73 of SEQ ID NO: 1
 residues 74 to 116 of SEQ ID NO: 1
 residues 117 to 185 of SEQ ID NO: 1
 residues 186 to 248 of SEQ ID NO: 1
 residues 29 to 73 of SEQ ID NO: 3
 10 residues 74 to 116 of SEQ ID NO: 3
 residues 117 to 185 of SEQ ID NO: 3
 residues 186 to 248 of SEQ ID NO: 3
 residues 1 to 32 of SEQ ID NO: 5
 residues 33 to 75 of SEQ ID NO: 5
 15 residues 76 to 144 of SEQ ID NO: 5
 residues 145 to 210 of SEQ ID NO: 5
 residues 34 to 80 of SEQ ID NO: 7
 residues 81 to 140 of SEQ ID NO: 7
 residues 33 to 79 of SEQ ID NO: 8
 20 residues 80 to 119 of SEQ ID NO: 8
 residues 120 to 161 of SEQ ID NO: 8
 residues 32 to 91 of SEQ ID NO: 21
 residues 25 to 84 of SEQ ID NO: 22
 residues 29 to 94 of SEQ ID NO: 24
 25 residues 31 to 85 of SEQ ID NO: 25
 residues 1 to 23 of SEQ ID NO: 26
 residues 1 to 17 of SEQ ID NO: 27
 residues 1 to 28 of SEQ ID NO: 28;
- (ii) a homologue of (i);
- 30 (iii) a polypeptide containing a relative cysteine spacing of C-2X-C-3X-C-(10-12)X-C-3X-C-3X-C wherein X is any amino acid residue, and C is cysteine;
- (iv) a polypeptide containing a relative cysteine and tyrosine/phenylalanine spacing of Z-2X-C-3X-C-(10-12)X-C-3X-C-3X-Z wherein X is any amino acid residue, and C is cysteine, and Z is tyrosine or phenylalanine;

- (v) a polypeptide containing a relative cysteine spacing of C-3X-C-(10-12)X-C-3X-C wherein X is any amino acid residue, and C is cysteine;
 - (vi) a polypeptide with substantially the same spacing of positively charged residues relative to the spacing of cysteine residues as (i); and
 - 5 (vii) a fragment of the polypeptide of any one of (i) to (vi) which has substantially the same antimicrobial activity as (i).
2. A protein containing at least one polypeptide fragment according to claim 1, wherein said polypeptide fragment has a sequence selected from within a sequence comprising SEQ ID NO: 1, SEQ ID NO: 3 or SEQ ID NO: 5
- 10 3. A protein having a sequence selected from SEQ ID NO: 1, SEQ ID NO: 3 or SEQ ID NO: 5.
4. An isolated or synthetic DNA encoding a polypeptide fragment according to claim 1.
5. The DNA according to claim 4, wherein said DNA has a sequence selected from SEQ ID NO: 2, SEQ ID NO: 4 or SEQ ID NO: 6.
- 15 6. A DNA construct which includes a DNA according to claim 4 operatively linked to elements for the expression of said encoded protein.
7. A transgenic plant harbouring a DNA construct according to claim 6.
8. The transgenic plant according to claim 7, wherein said plant is a monocotyledonous plant or a dicotyledonous plant.
- 20 9. The transgenic plant according to claim 7, wherein said plant is selected from maize, banana, peanut, field peas, sunflower, tomato, canola, tobacco, wheat, barley, oats, potato, soybeans, cotton, carnations, roses, or sorghum.
10. Reproductive material of a transgenic plant according to claim 7.
11. A composition comprising an antimicrobial protein according to claim 1 together with
- 25 an agriculturally-acceptable carrier diluent or excipient.
12. A composition comprising an antimicrobial protein according to claim 1 together with an pharmaceutically-acceptable carrier diluent or excipient.
13. A method of controlling microbial infestation of a plant, the method comprising:
- 30 i) treating said plant with an antimicrobial protein according to claim 1 or a composition according to claim 11; or
- ii) introducing a DNA construct according to claim 6 into said plant.
14. A method of controlling microbial infestation of a mammalian animal, the method comprising treating the animal with an antimicrobial protein according to claim 1 or a composition according to claim 12.

15. The method of claim 14, wherein said mammalian animal is a human.
16. A method of preparing an antimicrobial protein, which method comprises the steps of:
 - a) obtaining or designing an amino acid sequence which forms a helix-turn-helix structure;
 - 5 b) replacing individual residues to achieve substantially the same distribution of positively charged residues and cysteine residues as in one or more of the amino acid sequences shown in Figure 4;
 - c) synthesising a protein comprising said amino acid sequence chemically or by recombinant DNA techniques in liquid culture; and
 - 10 d) if necessary, forming disulphide linkages between said cysteine residues.

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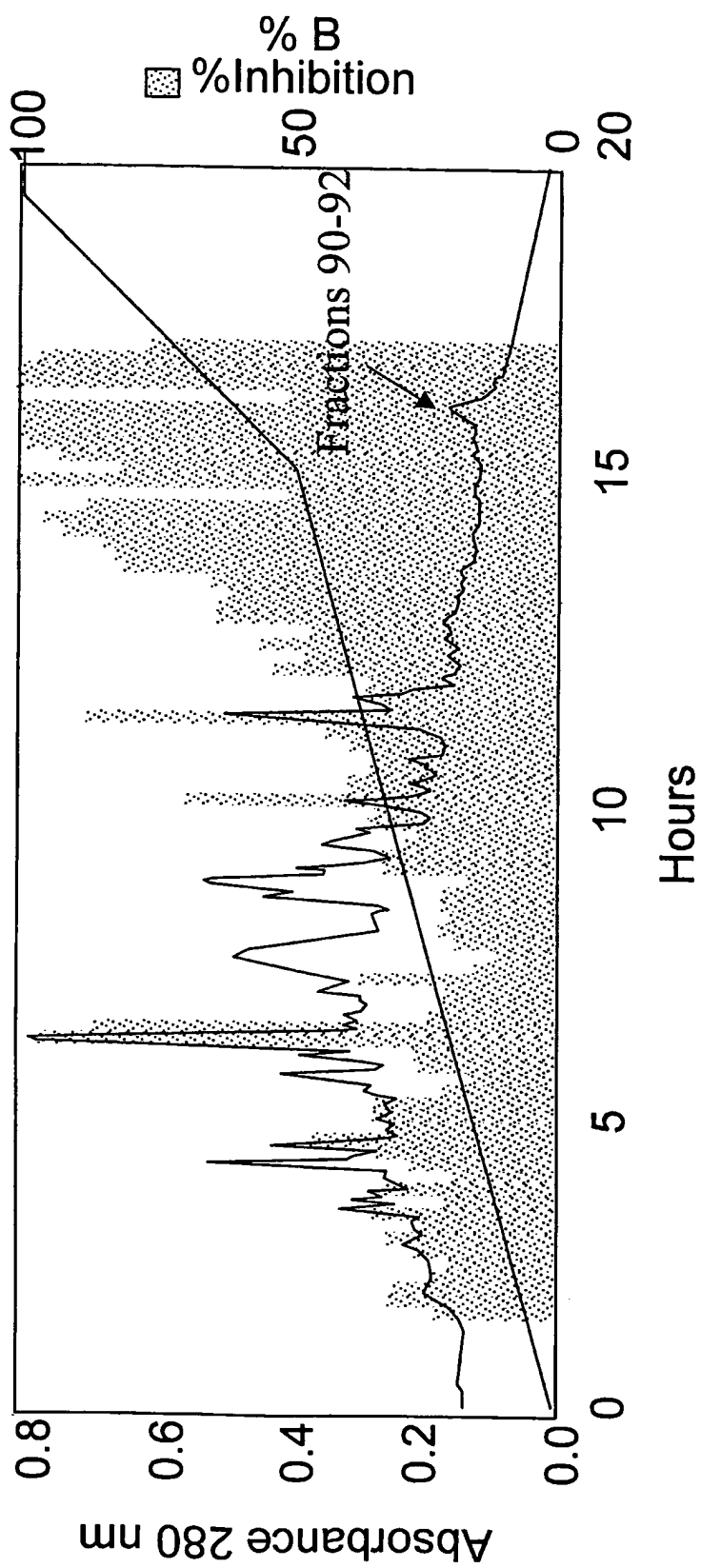


Fig. 1

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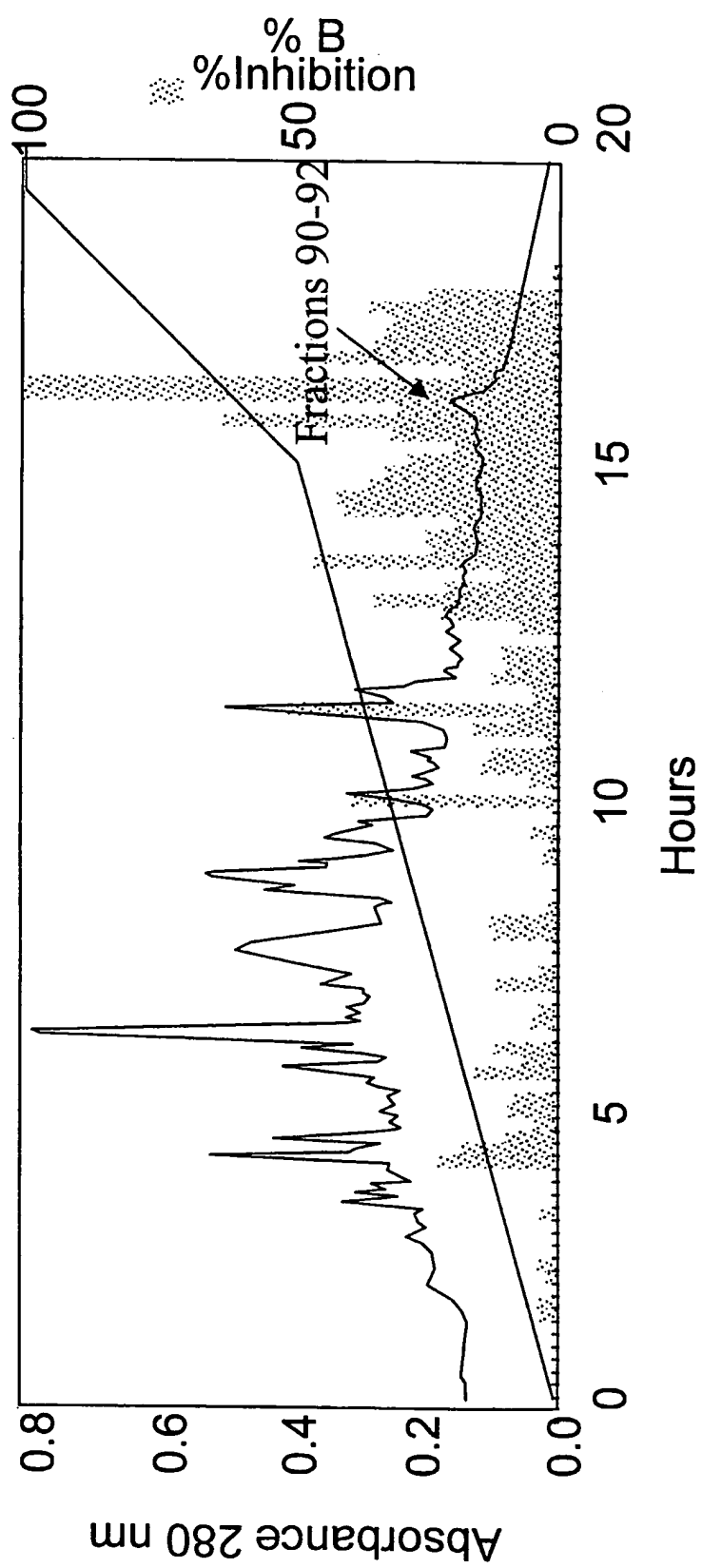


Fig. 2

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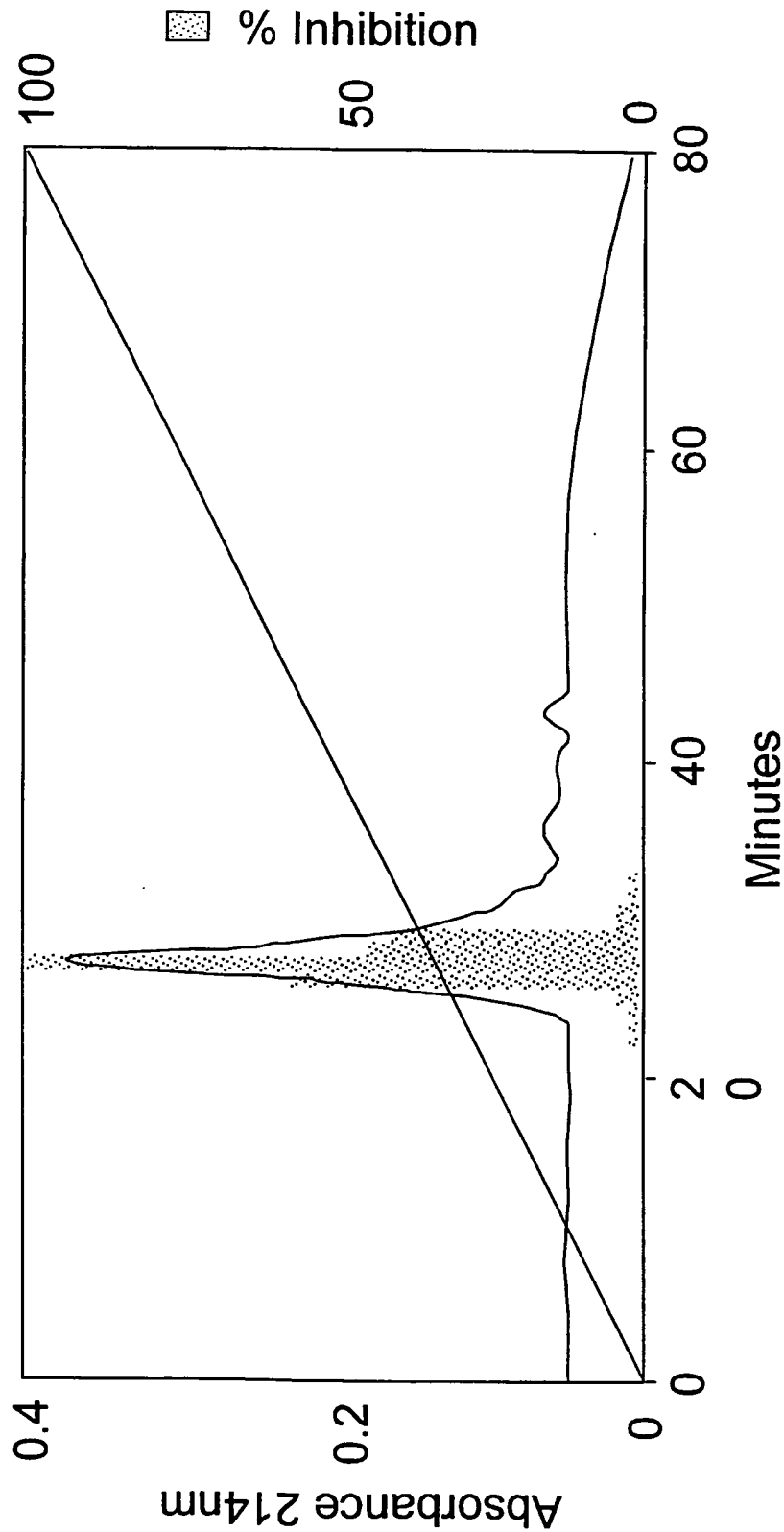


Fig. 3

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Mi2a	1	SEFDRQEYEECKRQCMQLE-TSG-QMRRRVSQCD	32
Mi2b	1	NQEDPQTECQQCQRRCRQQE-SGPRQQQYQRRCK	34
Mi2c	1	NRQDPQQQYEQCQKHCCORRE-TEPRHMQTCCQRCE	35
Mi2d	1	KRDPQQREYEDCRRRCRQQE---PRQQHQCQLRCR	32
Cocoa-a	1	YERDPQQYEQCQRRCESEA-TEEREQECCQRCE	34
Cocoa-b	1	LQRQYQQCQGRCCQEQQ-QGQREQQCCQRKCW	30
Cotton-a	1	GDDPPKRVEDCRRRCRCEWDT-RGQKEQQCCCESCK	34
Cotton-b	1	PEDPQRRYEECCQCECRQQE---ERQQPQCCQRCCL	31
Cotton-c	1	SQRQFQECQQCHCHQQE-QRPEKKQQCVRECR	30
maize glb1_0 fr	1	EDDNHHHGGHKSGRCVRRCEDR---PWHQRPRCCLEQCR	36
barley glob fra	1	HDDEDDRRGGHSLQQCVQRCRQER--PRYSHARCVCQECR	37
Peanut-a	1	TENP--CAQRCLQSCQQE--PDDLKQKACESRCT	30
alpha conglycin	1	ENP--KHNKCLQSCNSER--DSYRNQACHARC	29
SsAMP1 partial	1	VKEDHQFETRGEILECYRLCQQQ	23
SsAMP2 partial	1	QKHSQILGCCYLXCQQQL	17
SsAMP3 partial	1	LDPIRQQQLCQMRCCQQQEKD-PRQQQQCK	28

Fig. 4(1/2)

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Mi2a	33 KR FEED IDWSKYD	45
Mi2b	35 EI CEEEY	43
Mi2c	36 RRYEKERKQKRYEEQQREDEEKYEERM KEDN	69
Mi2d	33 EQQRQHGRGDMNPNPQRGGSGRY EEGEEEQS	63
Cocoa-a	35 RE YKEQQRQEEE	47
Cocoa-b	31 EQ YKEQ ERGEHENYHNHKKNR SEEEEGQQR	60
Cotton-a	35 SQ YGEK DQQQRHR	47
Cotton-b	32 KR FEQE QQQ	40
Cotton-c	31 EK YQEN PWRGER	42
maize glb1	37 EEEREKRQERSRHEADRS GEGSS	60
barley glob	38 DDQQQHGRHEQEEEQGRGRGWHG EGEEE	66
Peanut-a	31 KLEYDPR C VYDTGATNQRHPPGERT--RGRQP	60
alpha conglycin	30 LLKVEKE EECE GEI PRPR PRPQHPER	55
SsAMP1 partial	23	23
SsAMP2 partial	17	17
SsAMP3 partial	28	28

Fig. 4 (2/2)

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Fig. 5

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Mi clone 1      1  MAINTSNLCSLFLLSL-FLLSTTVSLAE-----SEFDRQEEYEE      38
Mi clone 2      1  MAINTSNLCSLFLLSL-FLLSTTVSLAE-----SEFDRQEEYEE      38
Mi clone 3      0                                     0
cotton vicilin  1  MVRNKSACVVLLFSLFLSFGLLCSAKDFPGRRGDD-----      35
cocoa vicilin   1  MVISKSPFIVLIFSLLLSFALLCSGVSAYGRKQYER-----      36
      * . . *      * . * * * * * . . .
Mi clone 1      39  CKRQCMQLETSGQMRRRCVVSQCDKRFEEDIDWSKYDNQEDPQTECQ      83
Mi clone 2      39  CKRQCMQLETSGQMRRRCVVSQCDKRFEEDIDWSKYDNQDDPQTdCQ      83
Mi clone 3      42  QCMQLETSGQMRRRCVVSQCDKRFEEDIDWSKYDNQEDPQTECQ      83
cotton vicilin  36  -----DPPKRYE      42
cocoa vicilin  37  -----DPRQQYE      43
      **
Mi clone 1      84  QCRRRCRQQESGPRQQYCQRRCKEICEEEEEYNRQR--DPQQQY      126
Mi clone 2      84  QCRRRCRQQESGPRQQYCQRRCKEICEEEEEYNRQR--DPQQQY      126
Mi clone 3      84  QCRRRCRQQESdPRQQYCQRRCKEICEEEEEYNRQR--DPQQQY      126
cotton vicilin  43  DCRRRCCEWDTRGQKEQQQCEESCKSQYGEKDQQQRHRRPEDPQRRY      87
cocoa vicilin  44  QCRRRCCESEATEEREQEQQCEQRCEREYKEQQRQQ--EEEELQRQY      85
      * . ***      . . . * * * * . . . * . . .

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Fig. 6 (1/6)

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Mi clone 1      127 EQCQKhCQRRETEPRHMQTCCQRCERRYEKEKRKQCKRYEEQQRE 171
Mi clone 2      127 EQCQeRCQRhETEPHMQTCCQRCERRYEKEKRKQCKRYEEQQRE 171
Mi clone 3      127 EQCQKRCCQRRETEPRHMQICQQRCERRYEKEKRKQCKRYEEQQRE 171
cotton vicilin 88 EECQCECRQEE--RQPPQCCQRCCLKRFEQEQQ----- 118
cocoa vicilin 86 QQCCGRCCQEQQGQREQQCCQRKCWEQY-KEQ----- 116
    ..** * . . . * . . . . . . . . . . . . . . . . . . . . . . . .
Mi clone 1      172 DEEKYEERMKEEDNKRDPPQREYEDCCRRRCEQQE--PRQHQCCQI 214
Mi clone 2      172 DEEKYEERMKEEDNKRDPPQREYEDCCRRRCEQQE--PRQYQCCQR 214
Mi clone 3      172 DEEKYEERMKEgDNKRDPPQREYEDCCRRhCEQQE--PRlQYQCCQR 214
cotton vicilin 119 -----QSQRQFQCCQHCHQEQEQRPCKKQCCVR 146
cocoa vicilin 117 ----- 116

Mi clone 1      215 RCREQQRQHGRGGdMNPQRGSGRYEEGEEeQSDNPYF-DERS 258
Mi clone 2      215 RCREQQRQHGRGDLiNPQRGSGRYEEGEEKQSDNPYF-DERS 258
Mi clone 3      215 RqEQQRQHGRGDLMNPQRGSGRYEEGEEKQSDNPYF-DERS 258
cotton vicilin 147 ECREKY--QENPWRGEREEEAEEEETEEEGEEQEQSHNPFHF-HRRS 188
cocoa vicilin 117 -----ER-GEHENYHNHKKNRSEEEGQQRNNPYFFPKRRS 151
    ** * * * * * * * * * * * * * * * * * * * * * *

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Fig. 6 (2/6)

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Mi clone 1      259 LSTRFRTEEGHISVLENFYGRSKLLRALKNYRLVLLLEANPNAFVL 303
Mi clone 2      259 LSTRFRTEEGHISVLENFYGRSKLLRALKNYRLVLLLEANPNAFVL 303
Mi clone 3      259 LSTRFRTEEGHISVLENFYGRSKLLRALKNYRLVLLLEANPNAFVL 303
cotton vicilin 189 FQSRFREEHGNERFVLQRFASRHPILRGINEFRLSILEANPNTFVL 233
cocoa vicilin  152 FQTRFRDEEGNFKILQRFASNSPPLKGINDYRLAMFEANPNTFIL 196
      . *** * * . * . * . * . * . * . * . * . * . * . *
Mi clone 1      304 PTHLDADAILLVIGRGALKMIHhDNRESYNLECGDVIRIPAGTT 348
Mi clone 2      304 PTHLDADAILLVTGGRGALKMIHRDNRESYNLECGDVIRIPAGTT 348
Mi clone 3      304 PTHLDADAILLVIGRGALKMIHRDNRESYNLECGDVIRIPAGTT 348
cotton vicilin 234 PHHCDAEKIYLVTNNGRGTTLTFLTHENKESYNIVPGVVVKVPAGST 278
cocoa vicilin  197 PHHCDAEAIYFVTNGKGTITFTVTHENKESYNVQRTVVSVVPAAGST 241
      * * * * * * * * * * . . . . . * * * * * . . . . . *
Mi clone 1      349 FYLINRDNNERLHIAKFLQTI STPGQYKEFFPAGGQNPPEP YLSTF 393
Mi clone 2      349 FYLINRDNNERLHIAKFLQTI STPGQYKEFFPAGGQNPPEP YLSTF 393
Mi clone 3      349 FYLINRDNNERLHIAKFLQTI STPGQYKEFFPAGGQNPPEP YLSTF 393
cotton vicilin 279 VYLANQDNKEKLI IAVLHRPVNPNPGQFEFFPAGSQR PQSYLRAF 323
cocoa vicilin  242 VYVVSQDNQEKLT IAVLALPVNSPGKYELFFPAGNNKPE SYYGAF 286
      * . . ** * . * * * . . * * * . . * * * . . * * * .

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Fig. 6 (3/6)

Mi clone 1	394	SKEILEAALNTQT E klRGVf-----GQRE-GVIIRASQEIQIRELT	433
Mi clone 2	394	SKEILEAALNTQ a eRLRGVL-----GQRE-GVIISASQEIQIRELT	433
Mi clone 3	394	SKEILEAALNTQTERLRGVL-----GQRE-GVIIRASQEIQIRELT	433
cotton vicilin	324	SREILEPAFNTRSEQLDELFGRQSRRRQQGG-MFRKASQEIQIR	367
cocoa vicilin	287	SYEVLETVFNTQREKLEEILEEQRGQKRQQQGMRKAKPEQIR	331
		* * . ** . ** . * *	
Mi clone 1	434	RDDSESrwhHIRRGGESSRGPYNLFNKRPLYSNKYQAyEvKPED	478
Mi clone 2	434	RDDSESrrWhIRRGGESSRGPYNLFNKRPLYSNKYQAyEvKPED	478
Mi clone 3	434	RDDSESRRWHIRRGGESSRGPYNLFNKRPLYSNKYQAyEvKPED	478
cotton vicilin	368	ALSQEATSPREK-SGE--RFAFNLLSQTPRYSNQNGRFFeACPPE	409
cocoa vicilin	332	AISQQATSPHR-GE--RLAINLLSQSPVYSNQNGRFFeACPED	373
	 * * * * * . * * * * *	
Mi clone 1	479	YRQLQMDlSVFIANvTQGSMMGPFfENTRSTKVvvVASGEADvEM	523
Mi clone 2	479	YRQLQMDvSVFIANIITQGSMMGPFfENTRSTKVvvVASGEADvEM	523
Mi clone 3	479	YRQLQMDvSVFIANIITQGSMMGPFfENTRSTKVvvVASGEADvEM	523
cotton vicilin	410	FRQLRDINVTVSALQLNQGSIFVPHYNSKATFvILvTEGNgyAEm	454
cocoa vicilin	374	FSQFQNMDVAVSafkLNQGAIfVPHYNSKATFVVFTDgYGyaQM	418
		* * * * * * * * * * * * *	

Fig. 6 (4/6)

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Mi clone 1      524 ACPHLSGRHGGRGGGKRHEEEED-----VHYEQVRARLSKREAIV 563
Mi clone 2      524 ACPHLSGRHGGRrggkrrHEEEED-----VHYEQVkARLSKREAIV 563
Mi clone 3      524 ACPHLSGRHGGRGGGKRHEEEEE-----VHYEQVRARLSKREAIV 563
cotton vicilin 455 VSPHLPRQSSYEEEEEEDEEEEQE-----VHYEQVRARLSKREAIV 499
cocoa vicilin  419 ACPHLSRQSQSGSRQDRREQE-----TFGEFQQVKAPLSPGD 463
                .***          * . . . .
                .***          * . . . .

Mi clone 1      564 ---VLAGHPVVFVSSGNENLLFAFGINAQNNHEN-----FLAGR 600
Mi clone 2      564 ---VpvGHPVVFVSSGNENLLFAFGINAQNNHEN-----FLAGR 600
Mi clone 3      564 ---VLAGHPVVFVSSGNENLLFAFGINAQNNHEN-----FLAGR 600
cotton vicilin 500 IFVVPANFPVTFVASQNQNLRMTGFGLYNQININPDHNQRI FVAGK 544
cocoa vicilin  464 VFVAPAGHAVTFFASKDQPLNAVAFGLNAQN-----NQRIFLAGR 503
                . * * * . * * * . * * * . * * * .

Mi clone 1      601 ERNVLQQIEPQAMELAFAAPRKEVEEsFNSQ-DqSIFFPGPRQHQQ 645
Mi clone 2      601 ERNVLQQIEPQAMELAFAAPRKEVEEELFNSQ-DESIFFPGPRQHQQ 645
Mi clone 3      601 ERNVLQQIEPQAMELAFAAsRKEVEEELFNSQ-DESIFFPGPRQHQQ 645
cotton vicilin 545 INHVRQ-WDSQAKELAFGVSSRLVDEIFNSNPQES-YF-VSRQQR 587
cocoa vicilin  504 -----PFFLNHKQNTN 514
                . * . . .

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Fig. 6 (5/6)

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Mi clone 1	646	QSPRSTKQQQPLVSILDFVGF	666
Mi clone 2	646	QSPRSTKQQQPLVSILDFVGF	666
Mi clone 3	646	QSPRSTKQQQPLVSILDFVGF	666
cotton vicilin	588	ASE	590
cocoa vicilin	515	VIKFTVKASAY	525

Fig. 6 (6/6)

	1	10	20	30	40	47
MiAMP2c	<u>RQRDPQQQYE</u>	<u>QCQKRCQRRE</u>	<u>TEPRHMQICQ</u>	<u>QRCERRYEKE</u>	<u>KRKQQQR</u>	
Gibrat method	CCCCCCCCCH	HHECCCCCCC	CCCCCEEEEC	CCCCCCHHH	HHHHHH	
Levin method	CCCCCHCCHH	HHHHHCHHT	HCSCCCECC	CHHTHHHHH	HHHCHH	
DPM method	CCCCCCCCCH	HHHHHHHHH	CHCCCHHEEH	HHHHHHHHH	HHHHCC	
SOPMA method	CCCCCHHHHH	HHHHHEECCC	CCCCHEEEE	EHHHHHHHH	HHHHHH	
PhD method	CCCCHHHHHH	HHHHHHHHH	CCCCCHHHH	HHHHHHHHH	HHHCCC	
Consensus	<u>CCCCCHCCHH</u>	<u>HHHHH-HH-</u>	<u>CCCC--EE-</u>	<u>-HHHHHHHH</u>	<u>HHHHHH</u>	

Fig. 7

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Fig. 8

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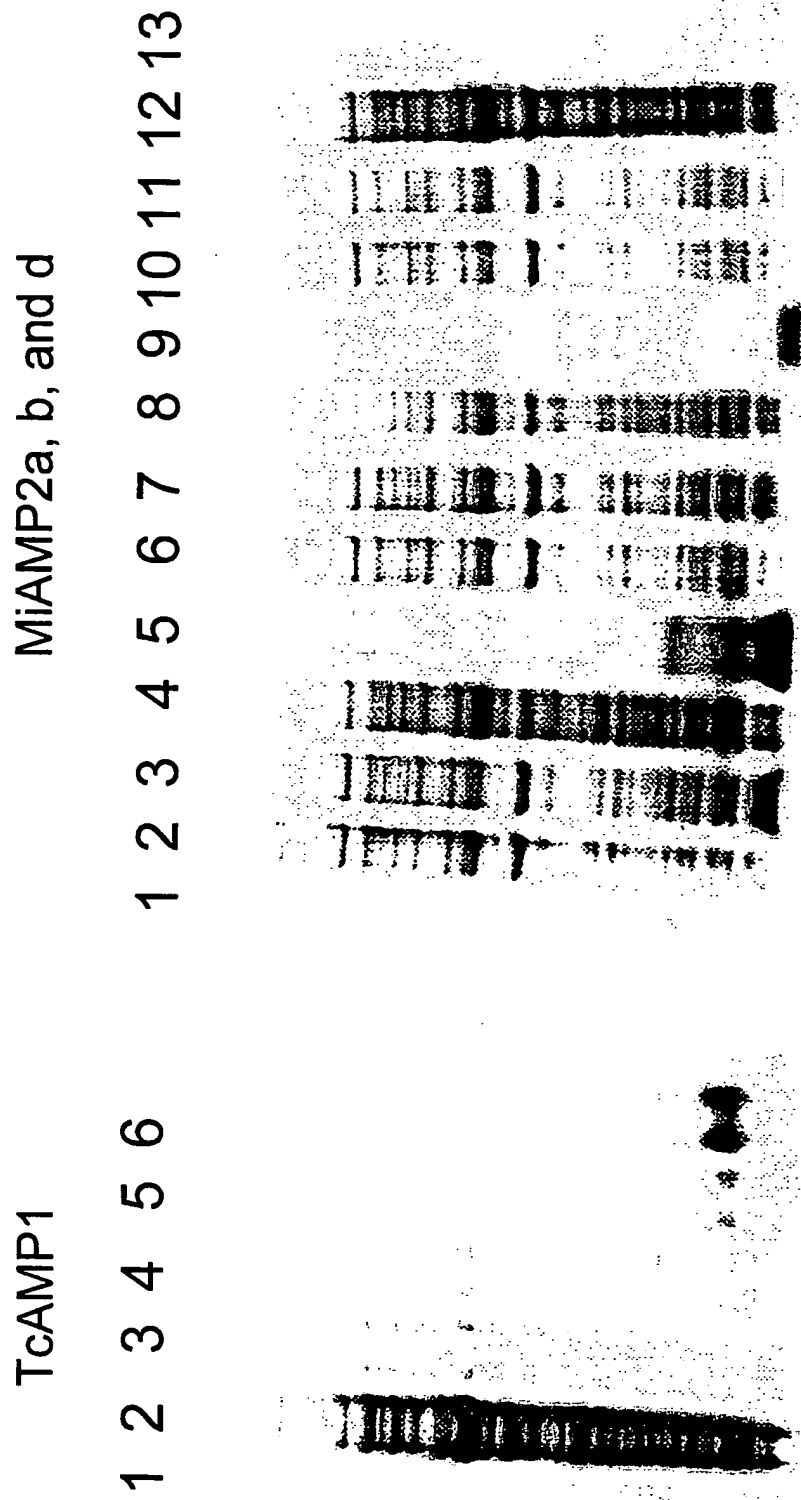


Fig. 9

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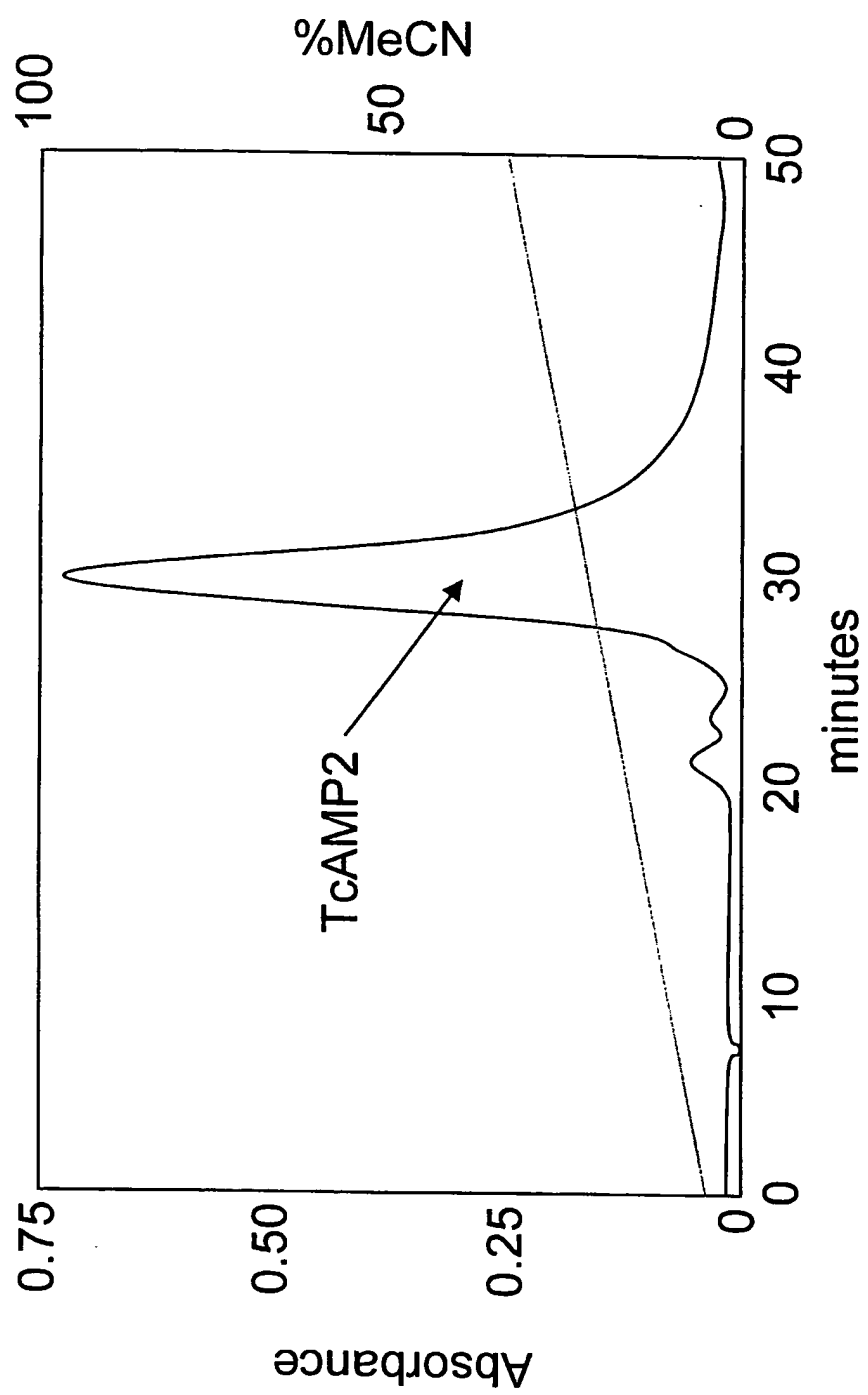


Fig. 10

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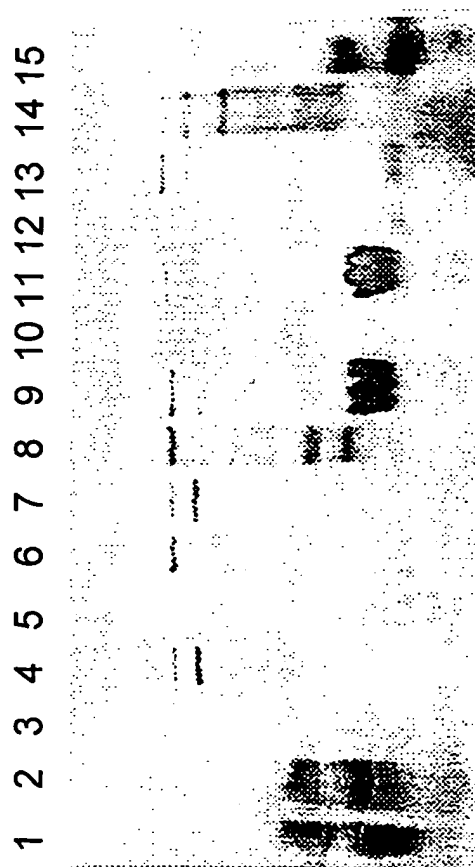


Fig. 11

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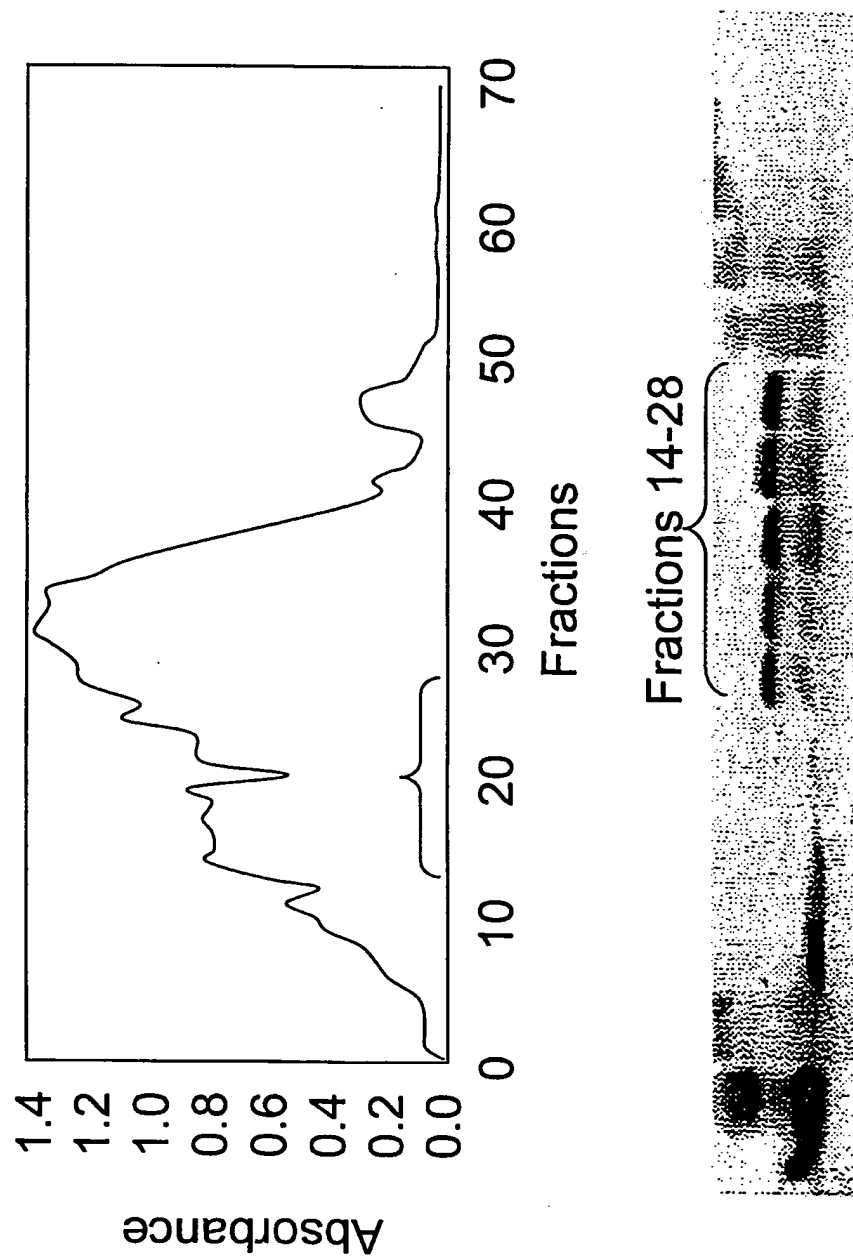


Fig. 12

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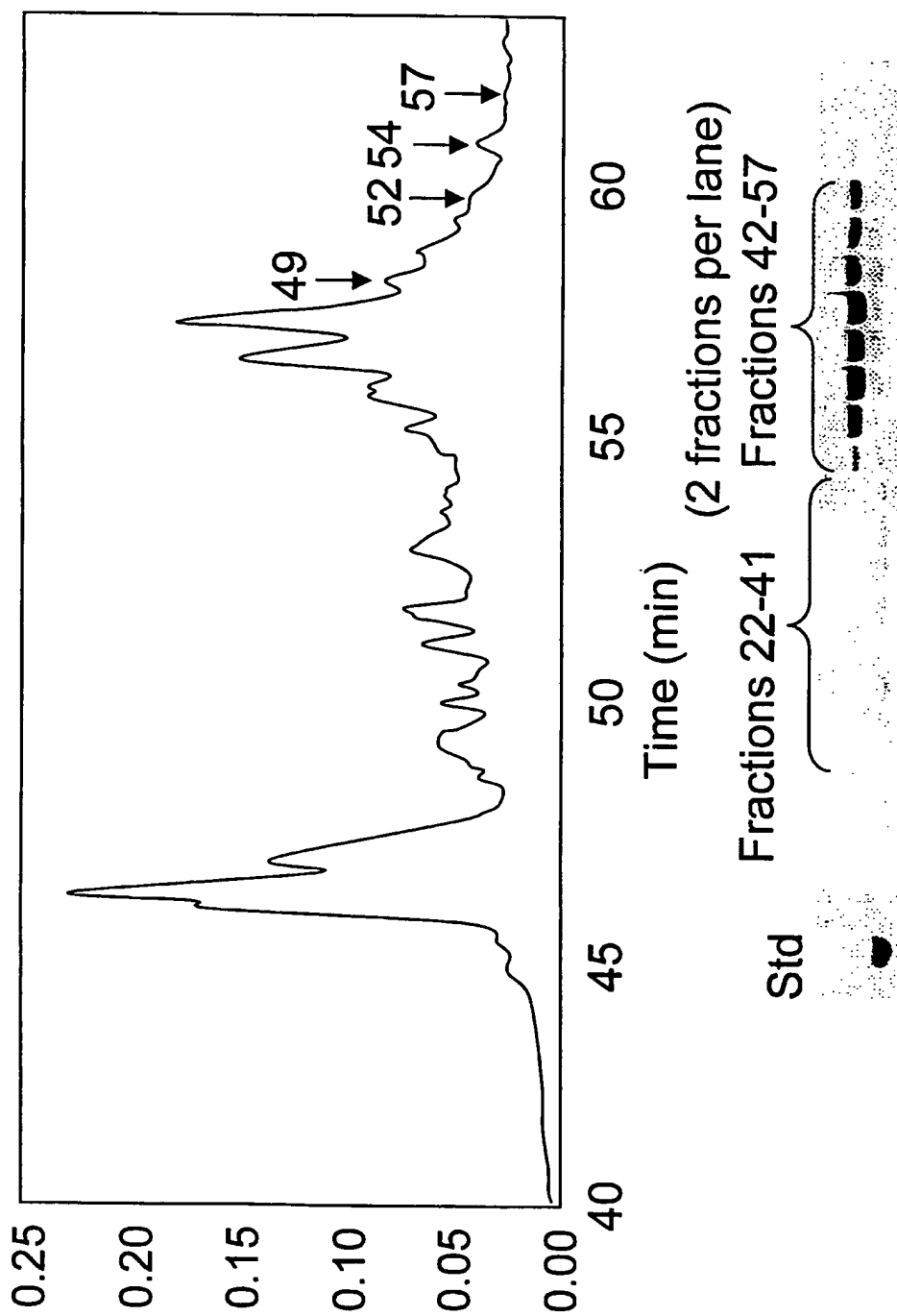


Fig. 13

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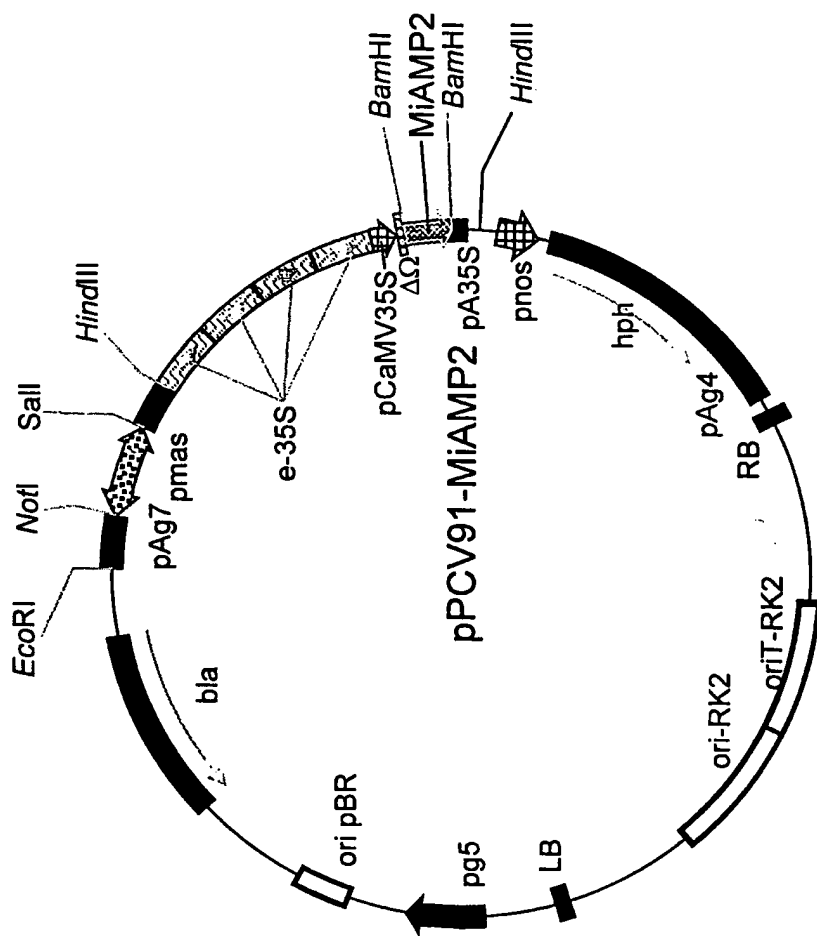


Fig. 14

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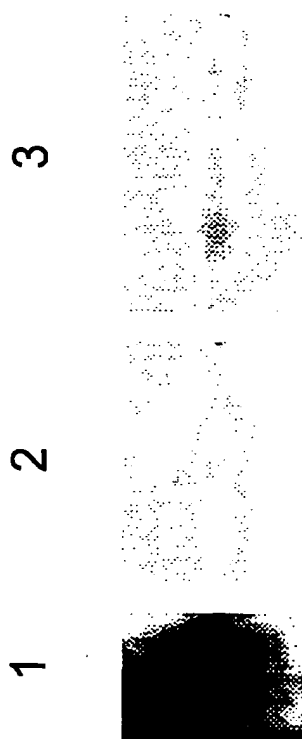


Fig. 15

INTERNATIONAL SEARCH REPORT

International Application No.
PCT/AU 97/00874

A. CLASSIFICATION OF SUBJECT MATTER		
Int Cl ⁶ : A01H 5/00, 5/10; A01N 37/18; C07K 4/10, 7/08, 14/415; C12N 15/29		
According to International Patent Classification (IPC) or to both national classification and IPC		
B. FIELDS SEARCHED		
Minimum documentation searched (classification system followed by classification symbols) CHEMICAL ABSTRACTS: See below		
Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched DGENE (Keywords as below)		
Electronic data base consulted during the international search (name of data base and, where practicable, search terms used) STN (Cas Online, DGENE) - CXXXCX(10, 12)CXXXC Swiss Prot, Genbank, EMBL, PIR-SEQ IDs 1, 3, 5, 7, 8, 21, 22, 24, 25, 26, 27, 28		
C. DOCUMENTS CONSIDERED TO BE RELEVANT		
Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 91/19801 (MARS UK LIMITED) 26 December 1991.	1, 4, 6, 11, 12
X	Plant Mol. Biol., Vol. 9, No. 6, 1987, Chlan et al., "Developmental biochemistry of cottonseed embryogenesis and germination XIX. Sequences and genomic organisation of the α -globulin (vicilin) genes of cottonseed", pages 533-46.	1, 4, 6, 11, 12
X	Plant Mol. Biol., Vol. 18, No. 6, 1992, McHenry and Fritz, "Comparison of the structure and nucleotide sequences of vicilin genes of cocoa and cotton raise questions about vicilin evolution", pages 1173-6.	1, 4, 6, 11, 12
<input checked="" type="checkbox"/> Further documents are listed in the continuation of Box C <input checked="" type="checkbox"/> See patent family annex		
<p>* Special categories of cited documents:</p> <p>"A" document defining the general state of the art which is not considered to be of particular relevance</p> <p>"E" earlier document but published on or after the international filing date</p> <p>"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)</p> <p>"O" document referring to an oral disclosure, use, exhibition or other means</p> <p>"P" document published prior to the international filing date but later than the priority date claimed</p> <p>"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention</p> <p>"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone</p> <p>"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art</p> <p>"&" document member of the same patent family</p>		
Date of the actual completion of the international search 20 February 1998		Date of mailing of the international search report 3 MAR 1998
Name and mailing address of the ISA/AU AUSTRALIAN INDUSTRIAL PROPERTY ORGANISATION PO BOX 200 WODEN ACT 2606 AUSTRALIA Facsimile No.: (02) 6285 3929		Authorized officer CHRISTOPHER LUTON Telephone No.: (02) 6283 2256

INTERNATIONAL SEARCH REPORT

International Application No.

PCT/AU 97/00874

C (Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT		
Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	Genetics, Vol. 129, No. 3, 1991, Belanger et al., "Molecular basis for allelic polymorphism of the maize Globulin-1 gene", pages 863-872.	1, 4, 6, 11, 12
X	Biochem. Genet., Vol. 27, No. 3-4, 1989, Kriz, "Characterization of embryo globulins encoded by the maize Glb genes", pages 239-251.	1, 4, 6, 11, 12
X	Mol. Gen. Genet., Vol. 239, No. 1-2, 1993, Heck et al., "Barley embryo globulin-1 gene, Beg1: characterization of cDNA, chromosome mapping and regulation of expression", pages 209-216.	1, 4, 6, 11, 12
X	J. Clin. Invest., Vol. 96, No. 4, 1995, Burks et al., "Recombinant peanut allergen Ara h1 expression and IgE binding in patients with peanut hypersensitivity", pages 1715-1721.	1, 4, 6, 11, 12
X	Plant Mol. Biol., Vol. 15, No. 1, 1990, Sebastiani et al., "Complete sequence of a cDNA of alpha subunit of soybean beta-conglycinin", pages 197-201.	1, 4, 6, 11, 12
X	Plant Mol. Biol., Vol. 7, No. 6, 1986, Chlan et al., "Developmental biochemistry of cottonseed embryogenesis and germination. XVIII. cDNA and amino acid sequences of members of the storage protein families.", pages 475-489.	1, 4, 6, 11, 12
X	TREMBL database entry, Accession No: Q41750, 1 November 1996.	1, 4, 6, 11, 12
X	EMBL database entry, Accession No: U28017, 7 August 1995.	1, 4, 6, 11, 12

INTERNATIONAL SEARCH REPORT

International Application No.

PCT/AU 97/00874

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☒ Claims Nos.: 1 (parts (vi) and (vii)) and 16
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
Due to the broad and indefinite scope of these claims, the International Search Authority finds that for economic reasons no meaningful search could be carried on said claims.
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a)

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

Information on patent family members

PCT/AU 97/00874

This Annex lists the known "A" publication level patent family members relating to the patent documents cited in the above-mentioned international search report. The Australian Patent Office is in no way liable for these particulars which are merely given for the purpose of information.

Patent Document Cited in Search Report				Patent Family Member			
WO	91/19801	AU,A,	79782/91	EP,A,	535053	GB,A,	9013016
		JP	5507846				